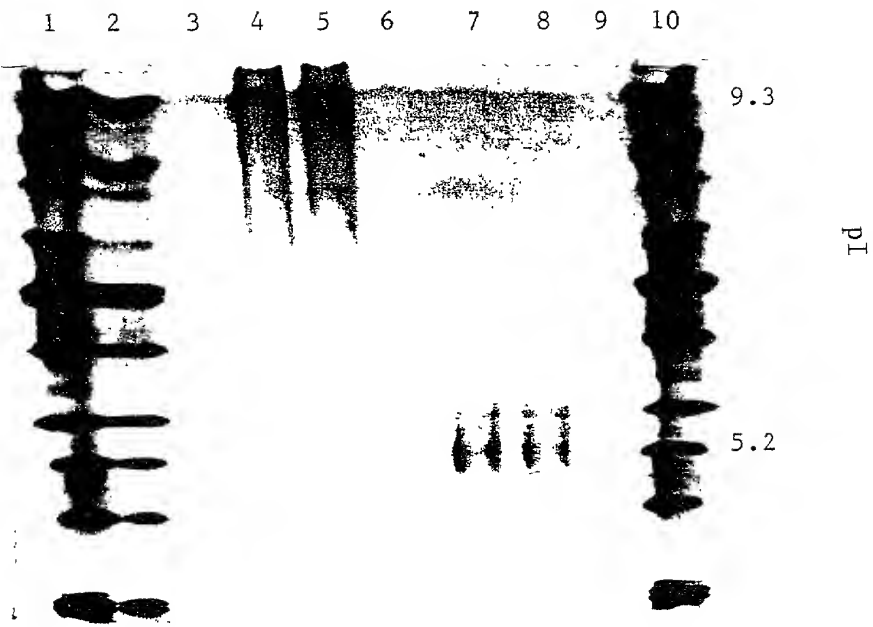


Figure 1



FOFETO* 228E2260

Figure 2

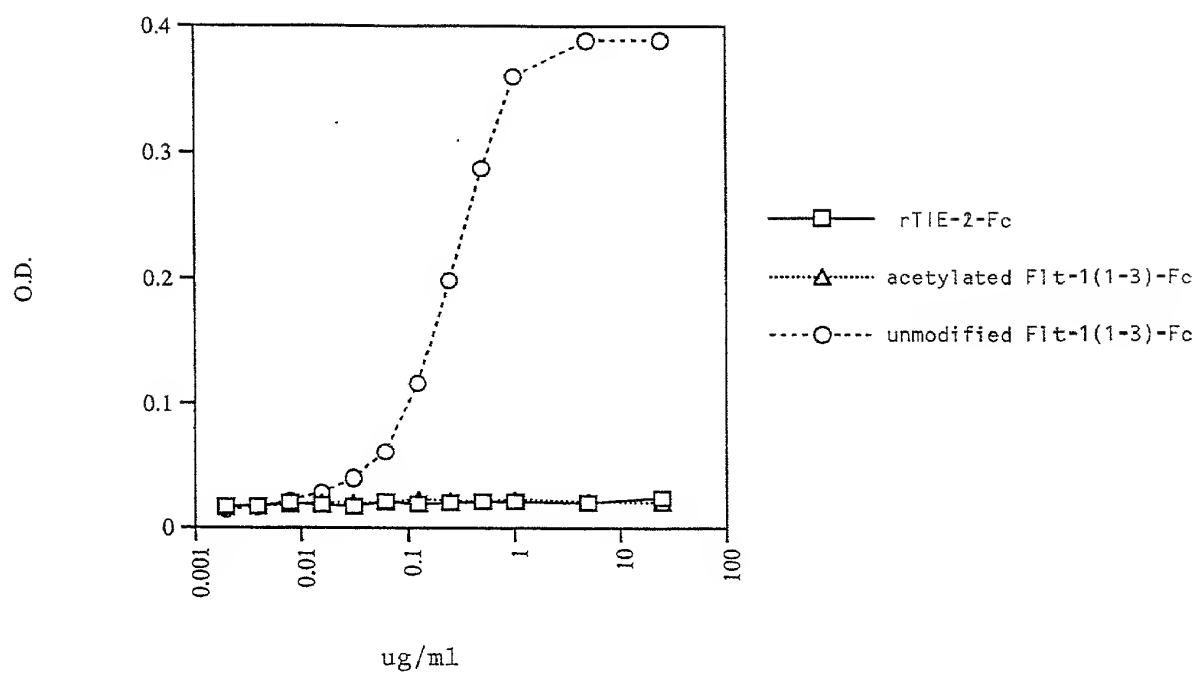


Figure 4

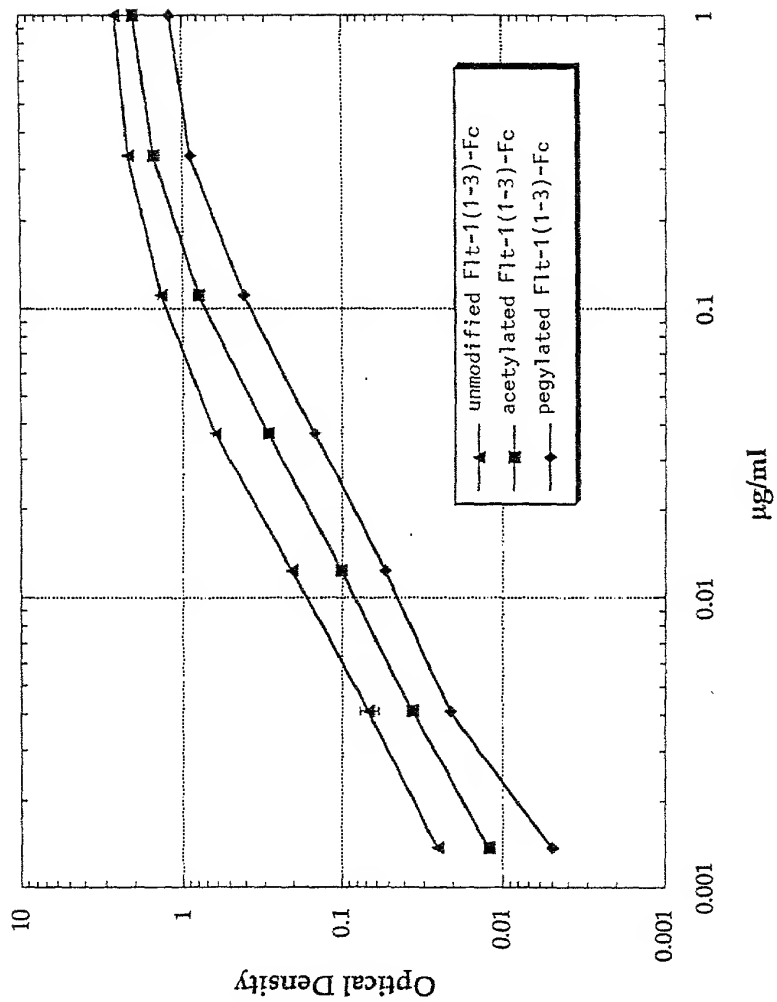


Figure 5

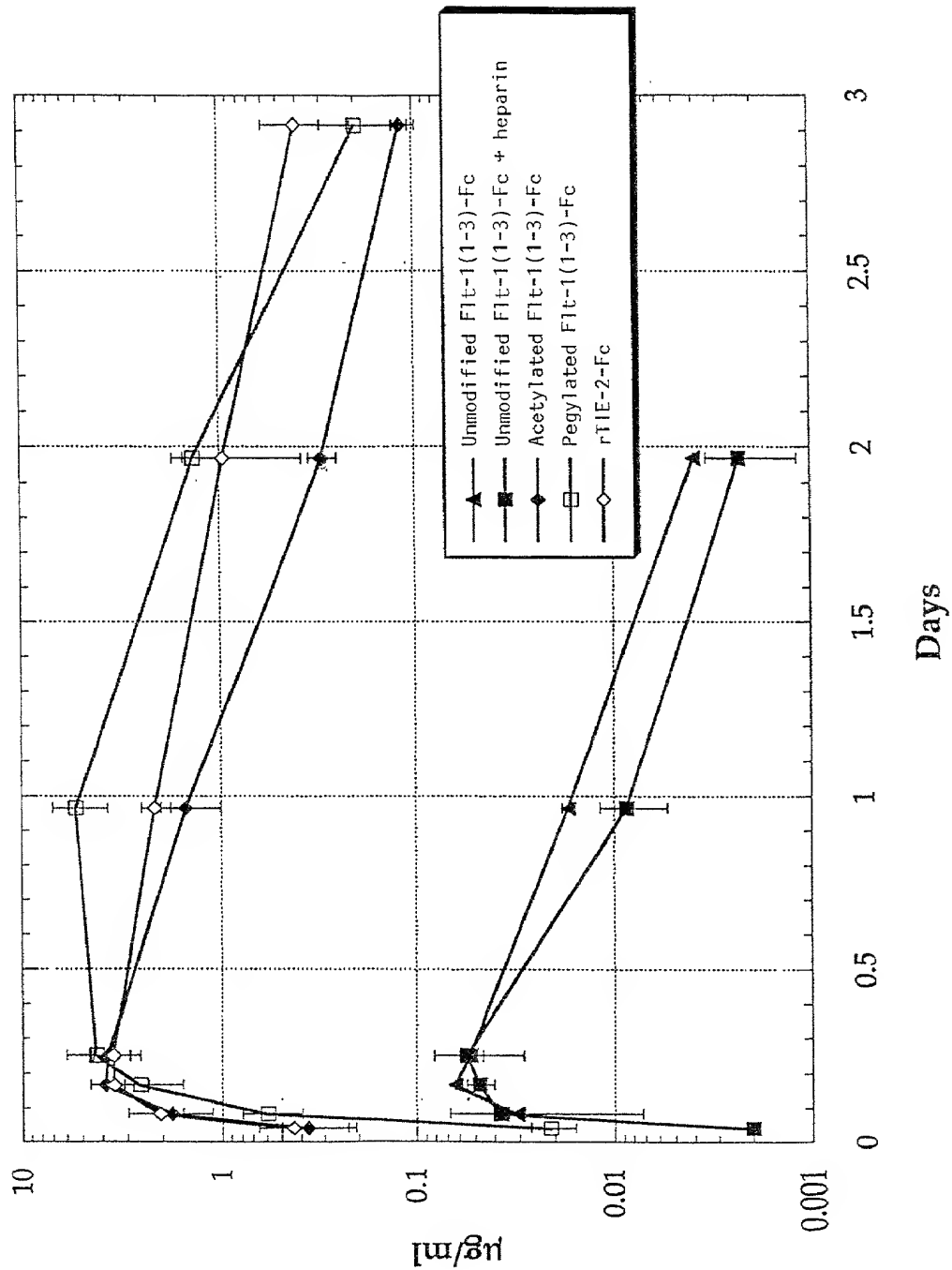


Figure 6A

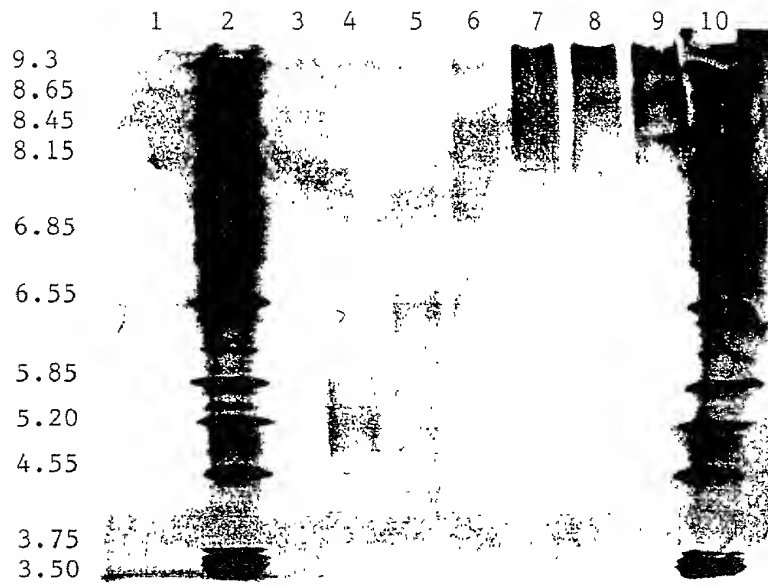


Figure 6B

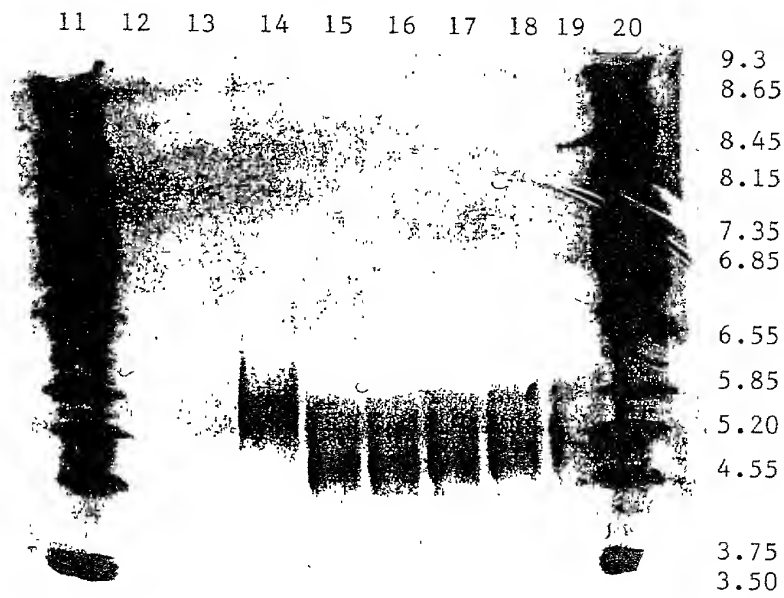


Figure 7

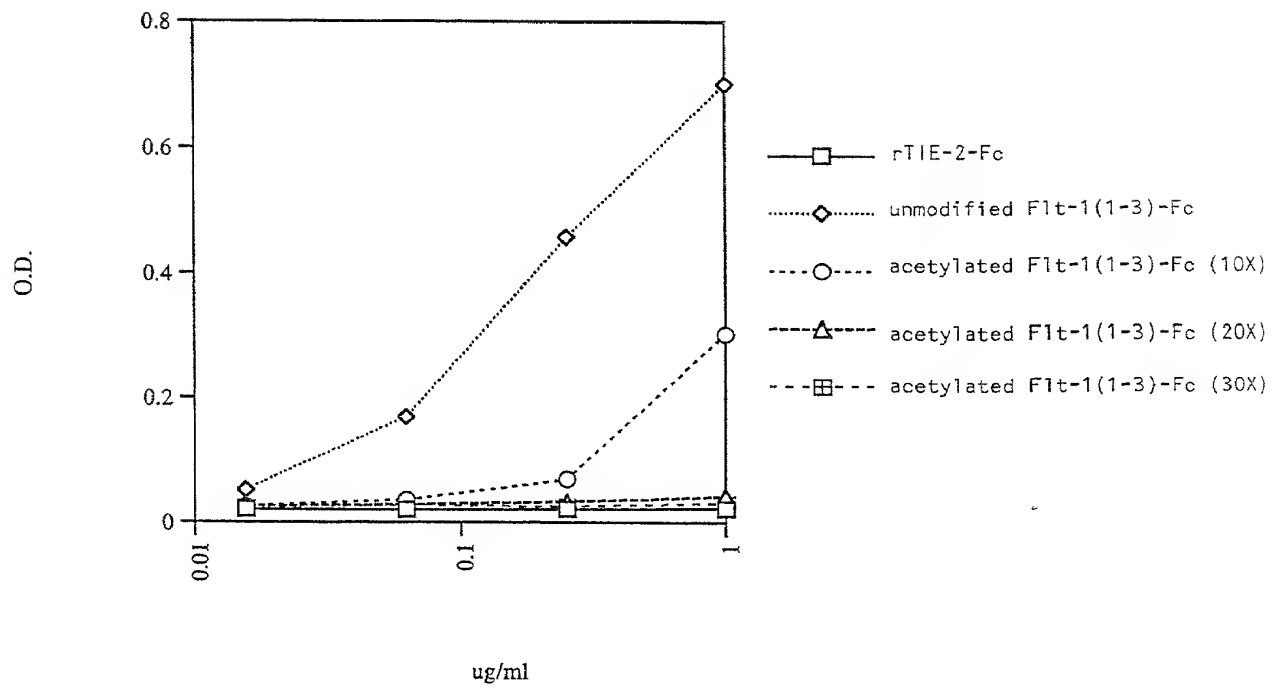
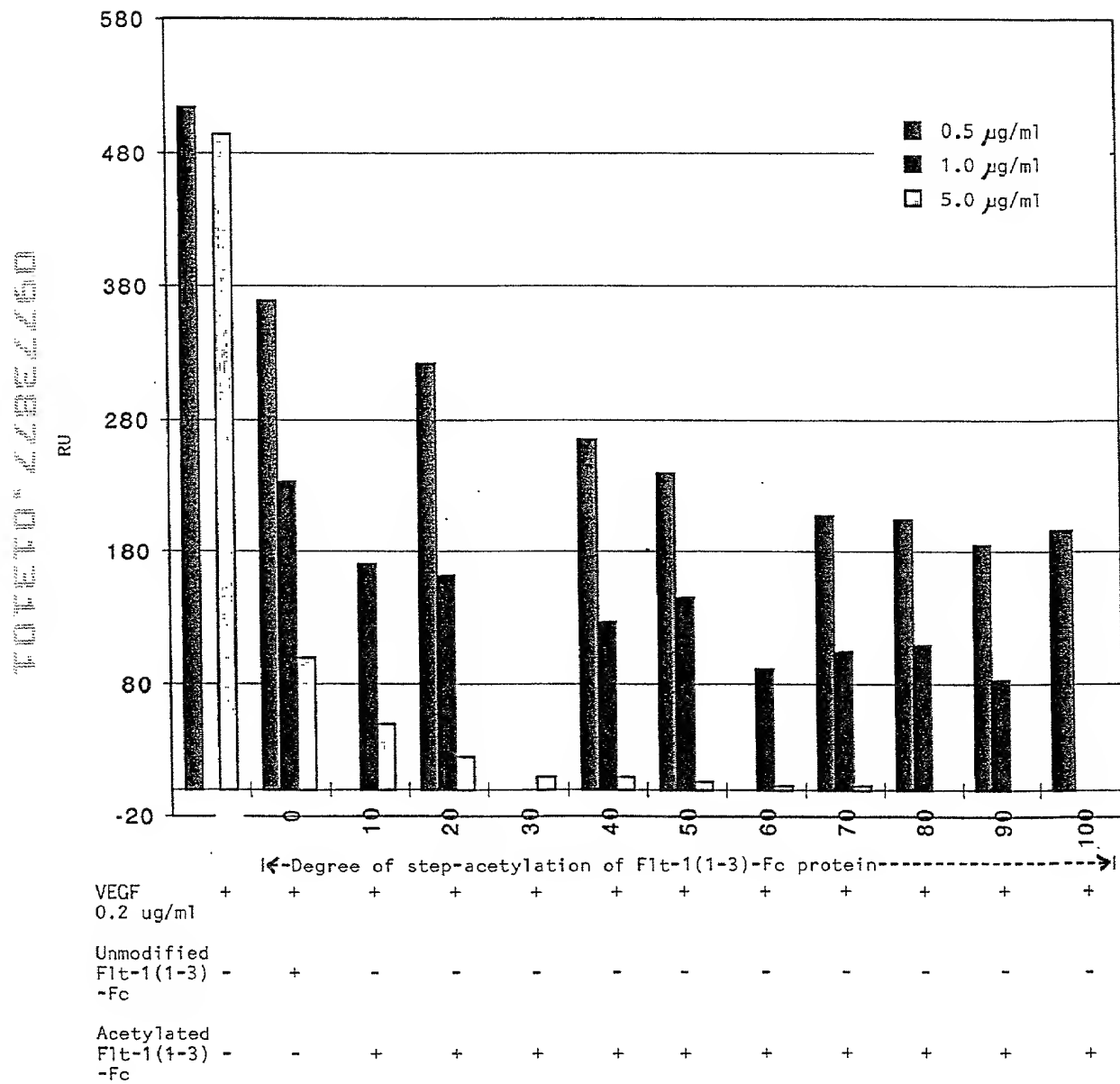


Figure 8



10				20				30				40				50				60			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ATG	GTC	AGC	TAC	TGG	GAC	ACC	GGG	GTC	CTG	CTG	TGC	GCG	CTG	CTC	AGC	TGT	CTG	CTT	CTC				
TAC	CAG	TCG	ATG	ACC	CTG	TGG	CCC	CAG	GAC	GAC	ACG	CGC	GAC	GAG	TCG	ACA	GAC	GAA	GAG				
Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Leu	Cys	Ala	Leu	Leu	Ser	Cys	Leu	Leu	Leu	>			
70				80				90				100				110				120			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
ACA	GGA	TCT	AGT	TCA	GGT	TCA	AAA	TTA	AAA	GAT	CCT	GAA	CTG	AGT	TTA	AAA	GGC	ACC	CAG				
TGT	CCT	AGA	TCA	AGT	CCA	AGT	TTT	AAT	TTT	CTA	GGA	CTT	GAC	TCA	AAT	TTT	CCG	TGG	GTC				
Thr	Gly	Ser	Ser	Ser	Gly	Ser	Lys	Leu	Lys	Asp	Pro	Glu	Leu	Ser	Leu	Lys	Gly	Thr	Gln	>			
130				140				150				160				170				180			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CAC	ATC	ATG	CAA	GCA	GGC	CAG	ACA	CTG	CAT	CTC	CAA	TGC	AGG	GGG	GAA	GCA	GCC	CAT	AAA				
GTG	TAG	TAC	GTT	CGT	CCG	GTC	TGT	GAC	GTA	GAG	GTT	ACG	TCC	CCC	CTT	CGT	CGG	GTA	TTT				
His	Ile	Met	Gln	Ala	Gly	Gln	Thr	Leu	His	Leu	Gln	Cys	Arg	Gly	Glu	Ala	Ala	His	Lys	>			
190				200				210				220				230				240			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TGG	TCT	TTG	CCT	GAA	ATG	GTG	AGT	AAG	GAA	AGC	GAA	AGG	CTG	AGC	ATA	ACT	AAA	TCT	GCC				
ACC	AGA	AAC	GGA	CTT	TAC	CAC	TCA	TTC	CTT	TCG	CTT	TCC	GAC	TCG	TAT	TGA	TTT	AGA	CGG				
Trp	Ser	Leu	Pro	Glu	Met	Val	Ser	Lys	Glu	Ser	Glu	Arg	Leu	Ser	Ile	Thr	Lys	Ser	Ala	>			
250				260				270				280				290				300			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TGT	GGA	AGA	AAT	GGC	AAA	CAA	TTC	TGC	AGT	ACT	TTA	ACC	TTG	AAC	ACA	GCT	CAA	GCA	AAC				
ACA	CCT	TCT	TTA	CCG	TTT	GTT	AAG	ACG	TCA	TGA	AAT	TGG	AAC	TTG	TGT	CGA	GTT	CGT	TTG				
Cys	Gly	Arg	Asn	Gly	Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr	Ala	Gln	Ala	Asn	>			
310				320				330				340				350				360			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CAC	ACT	GGC	TTC	TAC	AGC	TGC	AAA	TAT	CTA	GCT	GTA	CCT	ACT	TCA	AAG	AAG	AAG	AAG	GAA	ACA			
GTG	TGA	CCG	AAG	ATG	TCG	ACG	TTT	ATA	GAT	CGA	CAT	GGA	TGA	AGT	TTT	TTC	TTC	TTC	CTT	TGT			
His	Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val	Pro	Thr	Ser	Lys	Lys	Lys	Lys	Glu	Thr	>		
370				380				390				400				410				420			
*	*	*	*	*	*	*	*	*	*	*	*	*	*										

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Figure 10B

```

      550      560      570      580      590      600
      *      *      *      *      *      *
GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

      610      620      630      640      650      660
      *      *      *      *      *      *
GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA
Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

      670      680      690      700      710      720
      *      *      *      *      *      *
CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

      730      740      750      760      770      780
      *      *      *      *      *      *
AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>

      790      800      810      820      830      840
      *      *      *      *      *      *
AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AGA GCT TCC GTA AGG CGA
TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TCT CGA AGG CAT TCC GCT
Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Arg Ala Ser Val Arg Arg>

      850      860      870      880      890      900
      *      *      *      *      *      *
CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA
GCT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT
Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>

      910      920      930      940      950      960
      *      *      *      *      *      *
ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA
TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT
Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>

      970      980      990      1000      1010      1020
      *      *      *      *      *      *
TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT
AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>

      1030      1040      1050      1060      1070      1080
      *      *      *      *      *      *
GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC
CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val>

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REF ID: A66460

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Figure 10C

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      1090      1100      1110      1120      1130      1140
      *        *        *        *        *        *
TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA
AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr>

      1150      1160      1170      1180      1190      1200
      *        *        *        *        *        *
TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC
ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp>

      1210      1220      1230      1240      1250      1260
      *        *        *        *        *        *
GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC
CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr>

      1270      1280      1290      1300      1310      1320
      *        *        *        *        *        *
CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG
GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys>

      1330      1340      1350      1360      1370      1380
      *        *        *        *        *        *
TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
ACG TTC CAG AGG TTG TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys>

      1390      1400      1410      1420      1430      1440
      *        *        *        *        *        *
GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG
CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC CTA CTC GAC TGG TTC
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys>

      1450      1460      1470      1480      1490      1500
      *        *        *        *        *        *
AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG
TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG CTG TAG CGG CAC CTC
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu>

      1510      1520      1530      1540      1550      1560
      *        *        *        *        *        *
TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC
ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA GGG CAC GAC CTG AGG
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser>

      1570      1580      1590      1600      1610      1620
      *        *        *        *        *        *
GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG
CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG TCC ACC GTC GTC CCC
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly>

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      1630          1640          1650          1660          1670          1680
      *            *            *            *            *            *
AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC
TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser>

      1690          1700
      *            *            *            *
CTC TCC CTG TCT CCG GGT AAA TGA
GAG AGG GAC AGA GGC CCA TTT ACT
Leu Ser Leu Ser Pro Gly Lys ***>

```

Figure 11

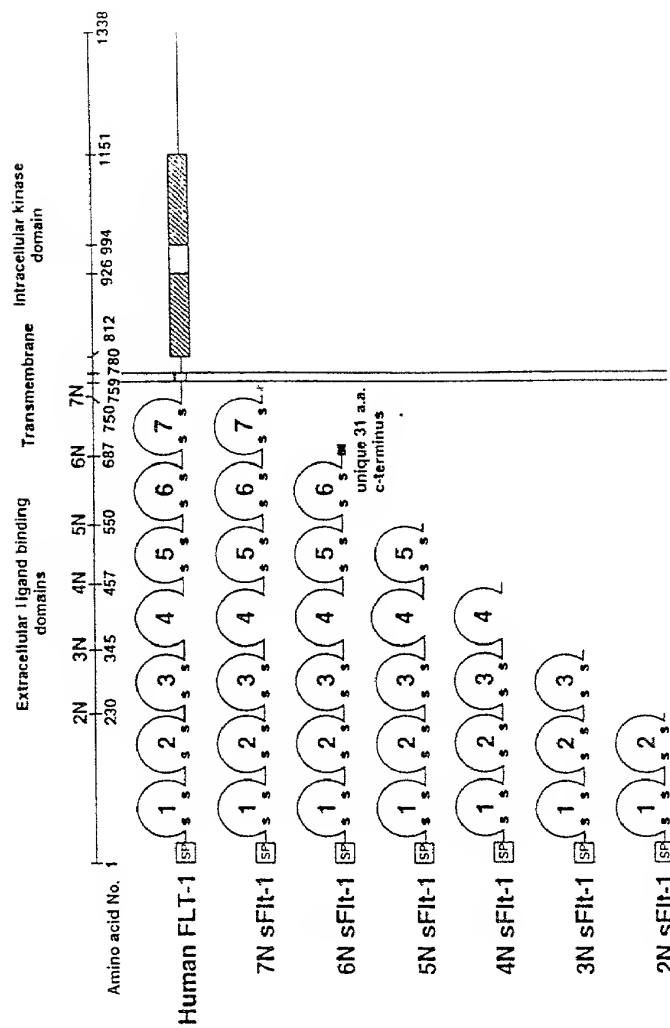


Figure 12A

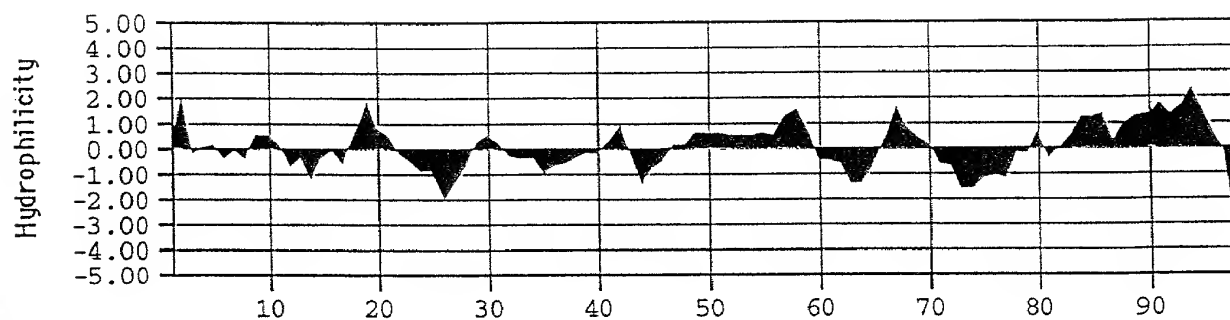
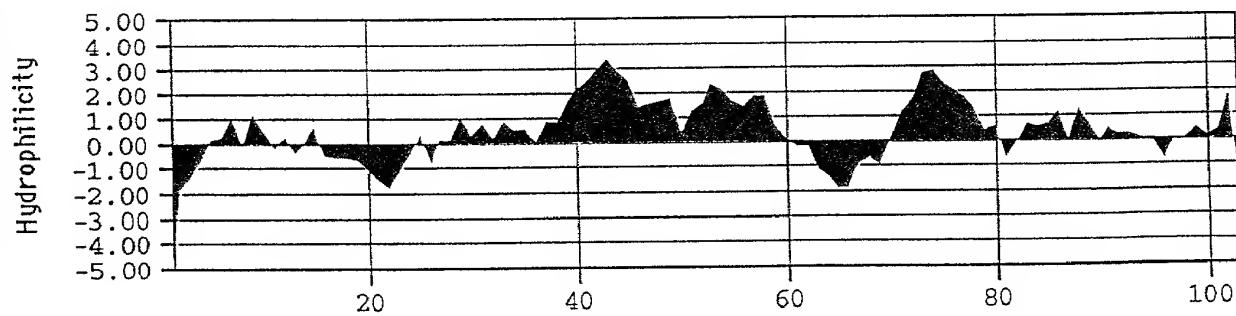


Figure 12B



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Figure 13A

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      10      20      30      40      50      60
      *      *      *      *      *      *
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>

      70      80      90      100      110      120
      *      *      *      *      *      *
ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG
TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC
Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>

      130      140      150      160      170      180
      *      *      *      *      *      *
CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA
GTG TAG TAC GTT CGT CCG GTC TGT GAC GTA GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT
His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>

      190      200      210      220      230      240
      *      *      *      *      *      *
TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC
ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG
Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>

      250      260      270      280      290      300
      *      *      *      *      *      *
TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC
ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG
Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>

      310      320      330      340      350      360
      *      *      *      *      *      *
CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA
GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC TTC CTT TGT
His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Lys Glu Thr>

      370      380      390      400      410      420
      *      *      *      *      *      *
GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT
CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA
Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>

      430      440      450      460      470      480
      *      *      *      *      *      *
GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT
CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA
Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>

      490      500      510      520      530      540
      *      *      *      *      *      *
ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT
TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA
Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>

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 Figure 13A
 10 20 30 40 50 60
 * * * * *
 ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
 TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG
 Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>
 70 80 90 100 110 120
 * * * * *
 ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG
 TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC
 Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>
 130 140 150 160 170 180
 * * * * *
 CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGG GAA GCA GCC CAT AAA
 GTG TAG TAC GTT CGT CCG GTC TGT GAC GTA GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT
 His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>
 190 200 210 220 230 240
 * * * * *
 TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC
 ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG
 Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>
 250 260 270 280 290 300
 * * * * *
 TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC
 ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG
 Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>
 310 320 330 340 350 360
 * * * * *
 CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA
 GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC TTC CTT TGT
 His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Lys Glu Thr>
 370 380 390 400 410 420
 * * * * *
 GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT
 CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA
 Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>
 430 440 450 460 470 480
 * * * * *
 GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT
 CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA
 Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>
 490 500 510 520 530 540
 * * * * *
 ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT
 TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA
 Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>

Figure 13B

```

      550      560      570      580      590      600
      *      *      *      *      *      *
GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

      610      620      630      640      650      660
      *      *      *      *      *      *
GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA
Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

      670      680      690      700      710      720
      *      *      *      *      *      *
CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

      730      740      750      760      770      780
      *      *      *      *      *      *
AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>

      790      800      810      820      830      840
      *      *      *      *      *      *
AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC
TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG
Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn>

      850      860      870      880      890      900
      *      *      *      *      *      *
ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT
TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA
Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr>

      910      920      930      940      950      960
      *      *      *      *      *      *
TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT
ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA
Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp>

      970      980      990      1000      1010      1020
      *      *      *      *      *      *
AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA
TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT
Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro>

      1030      1040      1050      1060      1070      1080
      *      *      *      *      *      *
GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr>

```

1090				1100				1110				1120				1130				1140			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	GAG	TAC	TAG	AGG
GAG	TAC	TAG	AGG	GCC	TGG	GGA	CTC	CAG	TGT	ACG	CAC	CAC	CAC	CTG	CAC	TCG	GTG	CTT	CTG	Leu	Met	Ile	Ser
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp						
1150				1160				1170				1180				1190				1200			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	GGA	CTC	CAG	TTC
AA	CTC	CAG	TTC	AAG	TTG	ACC	ATG	CAC	CTG	CCG	CAC	CTC	CAC	GTA	TTA	CGG	TTC	TGT	TTC	Pro	Glu	Val	Lys
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys								
1210				1220				1230				1240				1250				1260			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	GGC	GCC	CTC	CTC
GTC	CTG	ACC	GAC	TTA	CCG	TTC	CTC	ATG	TTC	ACG	TTC	CAG	AGG	TTG	TTT	CGG	GAG	GGT	CGG	Gln	Asp	Trp	Leu
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala								
1270				1280				1290				1300				1310				1320			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	GTC	CTG	ACC	GAC
GTC	CTG	ACC	GAC	TTA	CCG	TTC	CTC	ATG	TTC	ACG	TTC	CAG	AGG	TTG	TTT	CGG	GAG	GGT	CGG	Gln	Asp	Trp	Leu
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala								
1330				1340				1350				1360				1370				1380			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	GGG	TAG	CTC	TTT
TGG	TAG	CTC	TTT	TGG	TAG	AGG	TTT	CGG	TTT	CCC	GTC	GGG	GCT	CTT	GGT	GTC	CAC	ATG	TGG	Pro	Ile	Glu	Lys
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr								
1390				1400				1410				1420				1430				1440			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GAC	GGG	GGT	AGG
GCC	CTA	CTC	GAC	TGG	TTC	TTG	GTC	CAG	TCG	GAC	TGG	ACG	GAC	TGG	ACG	GAC	CAG	TTT	Leu	Pro	Pro	Ser	
Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys								
1450				1460				1470				1480											

Figure 13D

	1630		1640		1650		1660		1670								
	*	*	*	*	*	*	*	*	*								
GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	TGA
CGA	GAC	GTG	TTG	GTG	ATG	TGC	GTC	TTC	TCG	GAG	AGG	GAC	AGA	GGC	CCA	TTT	ACT
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	***>

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"0000" 0000

Figure 14A

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      10      20      30      40      50      60
      *      *      *      *      *      *
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>

      70      80      90      100      110      120
      *      *      *      *      *      *
ACA GGA TCT AGT TCC GGA GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC CCC GAA ATT
TGT CCT AGA TCA AGG CCT CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG GGG CTT TAA
Thr Gly Ser Ser Ser Gly Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile Pro Glu Ile>

      130      140      150      160      170      180
      *      *      *      *      *      *
ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA CCT AAC ATC
TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT GGA TTG TAG
Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val Thr Ser Pro Asn Ile>

      190      200      210      220      230      240
      *      *      *      *      *      *
ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA CGC ATA ATC
TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT GCG TAT TAG
Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile>

      250      260      270      280      290      300
      *      *      *      *      *      *
TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA GGG CTT CTG
ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT CCC GAA GAC
Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu>

      310      320      330      340      350      360
      *      *      *      *      *      *
ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA CAT CGA CAA
TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT GTA GCT GTT
Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr His Arg Gln>

      370      380      390      400      410      420
      *      *      *      *      *      *
ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC AAA TTA CTT AGA GGC
TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG TTT AAT GAA TCT CCG
Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val Lys Leu Leu Arg Gly>

      430      440      450      460      470      480
      *      *      *      *      *      *
CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG AGA GTT CAA ATG ACC
GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC TCT CAA GTT TAC TGG
His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr Arg Val Gln Met Thr>

      490      500      510      520      530      540
      *      *      *      *      *      *
TGG AGT TAC CCT GAT GAA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT
ACC TCA ATG GGA CTA CTT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA
Trp Ser Tyr Pro Asp Glu Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val>

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* * * * *
 CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT
 GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA
 Leu Thr Ile Asp Lys Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser>
 * * * * *
 GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC
 CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG
 Gly Pro Ser Phe Lys Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly>
 * * * * *
 GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG
 CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu>
 * * * * *
 GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG
 CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg>
 * * * * *
 ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC
 TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe>
 * * * * *
 AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG
 TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln>
 * * * * *
 TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT
 ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn>
 * * * * *
 GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC
 CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG TTT CGG GAG GGT CCG GGG TAG CTC TTT TGG
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr>
 * * * * *
 ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG
 TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT GGT GTC CAC ATG TGG GAC GGG GGT AGG GCC
 Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg>

Figure 14C

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      1090      1100      1110      1120      1130      1140
      *        *        *        *        *        *
GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC
CTA CTC GAC TGG TTC TTG GTC CAG TCG GAC TGG ACG GAC CAG TTT CCG AAG ATA GGG TCG
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser>

      1150      1160      1170      1180      1190      1200
      *        *        *        *        *        *
GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT
CTG TAG CGG CAC CTC ACC CTC TCG TTA CCC GTC GGC CTC TTG TTG ATG TTC TGG TGC GGA
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro>

      1210      1220      1230      1240      1250      1260
      *        *        *        *        *        *
CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC
GGG CAC GAC CTG AGG CTG CCG AGG AAG AAG GAG ATG TCG TTC GAG TGG CAC CTG TTC TCG
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser>

      1270      1280      1290      1300      1310      1320
      *        *        *        *        *        *
AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC
TCC ACC GTC GTC CCC TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His>

      1330      1340      1350
      *        *        *        *        *        *
TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
ATG TGC GTC TTC TCG GAG AGG GAC AGA GGC CCA TTT ACT
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys ***>

```

1090 1100 1110 1120 1130 1140
 1150 1160 1170 1180 1190 1200
 1210 1220 1230 1240 1250 1260
 1270 1280 1290 1300 1310 1320
 1330 1340 1350

Figure 15A

	10		20		30		40		50		60
*	*	*	*	*	*	*	*	*	*	*	*
ATG	GTC	AGC	TAC	TGG	GAC	ACC	GGG	GTC	CTG	CTG	TGC
TAC	CAG	TCG	ATG	ACC	CTG	TGG	CCC	CAG	GAC	ACG	CGC
Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Cys	Ala
											Leu
											Leu
											Leu>
	70		80		90		100		110		120
*	*	*	*	*	*	*	*	*	*	*	*
ACA	GGA	TCT	AGT	TCC	GGA	GGT	AGA	CCT	TTC	GTA	GAG
TGT	CCT	AGA	TCA	AGG	CCT	CCA	TCT	GGA	AAG	CAT	CTC
Thr	Gly	Ser	Ser	Ser	Gly	Gly	Arg	Pro	Phe	Val	Glu
											Met
											Tyr
											Ser
											Glu
											Ile
											Pro
											Glu
											Ile>
	130		140		150		160		170		180
*	*	*	*	*	*	*	*	*	*	*	*
ATA	CAC	ATG	ACT	GAA	GGA	AGG	GAG	CTC	GTC	ATT	CCC
TAT	GTG	TAC	TGA	CTT	CCT	TCC	CTC	GAG	CAG	TAA	GGG
Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro
											Cys
											Arg
											Val
											Thr
											Ser
											Pro
											Asn
											Ile>
	190		200		210		220		230		240
*	*	*	*	*	*	*	*	*	*	*	*
ACT	GTT	ACT	TTA	AAA	AAG	TTT	CCA	CTT	GAC	ACT	TTG
TGA	CAA	TGA	AAT	TTT	TTC	AAA	GGT	GAA	CTG	TGA	AAC
Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	Leu
											Ile
											Pro
											Asp
											Gly
											Lys
											Arg
											Ile
											Ile>
	250		260		270		280		290		300
*	*	*	*	*	*	*	*	*	*	*	*
TGG	GAC	AGT	AGA	AAG	GGC	TTC	ATC	ATA	TCA	AAT	GCA
ACC	CTG	TCA	TCT	TTC	CCG	AAG	TAG	TAT	AGT	TTA	CGT
Trp	Asp	Ser	Arg	Lys	Gly	Phe	Ile	Ile	Ser	Asn	Ala
											Thr
											Tyr
											Lys
											Glu
											Ile
											Gly
											Leu
											Leu>
	310		320		330		340		350		360
*	*	*	*	*	*	*	*	*	*	*	*
ACC	TGT	GAA	GCA	ACA	GTC	AAT	GGG	CAT	TTG	TAT	AAG
TGG	ACA	CTT	CGT	TGT	CAG	TTA	CCC	GTA	AAC	ATA	TTC
Thr	Cys	Glu	Ala	Thr	Val	Asn	Gly	His	Leu	Tyr	Lys
											Thr
											Asn
											Tyr
											Leu
											Thr
											His
											Arg
											Gln>
	370		380		390		400		410		420
*	*	*	*	*	*	*	*	*	*	*	*
ACC	AAT	ACA	ATC	ATA	GAT	GTC	CAA	ATA	AGC	ACA	CCA
TGG	TTA	TGT	TAG	TAT	CTA	CAG	GTT	TAT	TCG	TGT	GGT
Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro
											Arg
											Pro
											Val
											Lys
											Leu
											Leu
											Arg
											Gly>
	430		440		450		460		470		480
*	*	*	*	*	*	*	*	*	*	*	*
CAT	ACT	CTT	GTC	CTC	AAT	TGT	ACT	GCT	ACC	ACT	CCC
GTA	TGA	GAA	CAG	GAG	TTA	ACA	TGA	CGA	TGG	TGA	GGG
His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr	Pro
											Leu
											Asn
											Thr
											Arg
											Val
											Gln
											Met
											Thr>
	490		500		510		520		530		540
*	*	*	*	*	*	*	*	*	*	*	*
TGG	AGT	TAC	CCT	GAT	GAA	AAA	AAT	AAG	AGA	GCT	TCC
ACC	TCA	ATG	GGA	CTA	CTT	TTT	TTA	TTC	TCT	CGA	AGG
Trp	Ser	Tyr	Pro	Asp	Glu	Lys	Asn	Lys	Arg	Ala	Ser
											Val
											Arg
											Arg
											Arg
											Ile
											Asp
											Gln
											Ser>

TOP SECRET

Figure 15B

```

      550      560      570      580      590      600
      *      *      *      *      *      *
AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA ATG CAG AAC AAA GAC
TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT TAC GTC TTG TTT CTG
Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys Met Gln Asn Lys Asp>

      610      620      630      640      650      660
      *      *      *      *      *      *
AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA TCT GTT AAC ACC TCA
TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT AGA CAA TTG TGG AGT
Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys Ser Val Asn Thr Ser>

      670      680      690      700      710      720
      *      *      *      *      *      *
GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA
CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA CTG TTT TGA GTG TGT
Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr>

      730      740      750      760      770      780
      *      *      *      *      *      *
TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGC GGA CCG TCA GTC TTC CTC TTC CCC CCA
ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro>

      790      800      810      820      830      840
      *      *      *      *      *      *
AAA CCC AAG GAC ACC CTC ATG ATC TCC CGS ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC
TTT GGG TTC CTG TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp>

      850      860      870      880      890      900
      *      *      *      *      *      *
GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT
CAC TCG GTG CTT CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC GTA
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His>

      910      920      930      940      950      960
      *      *      *      *      *      *
AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC
TTA CGG TTC TGT TTC GGC GCC CTC CTC GTC ATG TTG TCG TGC ATG GCA CAC CAG TCG CAG
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val>

      970      980      990      1000      1010      1020
      *      *      *      *      *      *
CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC
GAG TGG CAG GAC GTG GTC CTG ACC GAC TTA CCG TTC CTC ATG TTC ACG TTC CAG AGG TTG
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn>

      1030      1040      1050      1060      1070      1080
      *      *      *      *      *      *
AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGC CAG CCC CGA GAA
TTT CGG GAG GGT CGG GGG TAG CTC TTT TGG TAG AGG TTT CGG TTT CCC GTC GGG GCT CTT
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu>

```


4

1090				1100				1110				1120				1130				1140			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	GGT	GTC	CAC	ATG
GGT	GTC	CAC	ATG	TGG	GAC	GGG	GGT	AGG	GCC	CTA	CTC	GAC	TGG	TTC	TTG	GTC	CAG	TCG	GAC	Pro	Gln	Val	Tyr
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	>			
1150				1160				1170				1180				1190				1200			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
AAC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	TGG	ACG	GAC	CAG
TGG	ACG	GAC	CAG	TTT	CCG	AAG	ATA	GGG	TCG	CTG	TAG	CGG	CAC	CTC	ACC	CTC	TCG	TTA	CCC	Thr	Cys	Leu	Val
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	>			
1210				1220				1230				1240				1250				1260			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	GTC	GGC	CTC	TTG
GTC	GGC	CTC	TTG	TTG	ATG	TTC	TGG	TGC	GGA	GGG	CAC	GAC	CTG	AGG	CTG	CCG	AGG	AAG	AAG	Gln	Pro	Glu	Asn
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	>			
1270				1280				1290				1300				1310				1320			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	GAG	ATG	TCG	TTC
GAG	ATG	TCG	TTC	GAG	TGG	CAC	CTG	TTC	TCG	TCC	ACC	GTC	GTC	CCC	TTG	CAG	AAG	AGT	ACG	Leu	Tyr	Ser	Lys
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	>			
1330				1340				1350				1360				1370				1380			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	AGG	CAC	TAC	GTA
AGG	CAC	TAC	GTA	CTC	CGA	GAC	GTG	TTG	GTG	ATG	TGC	GTC	TTC	TCG	GAG	AGG	GAC	AGA	GGC	Ser	Val	Met	His
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	>			
* GGT AAA TGA CCA TTT ACT Gly Lys ***>																							

Figure 16A

```

      10      20      30      40      50      60
      *      *      *      *      *      *
ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG GCG GAC GAG TCG ACA GAC GAA GAG
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu Leu Ser Cys Leu Leu Leu>

      70      80      90      100      110      120
      *      *      *      *      *      *
ACA GGA TCT AGT TCA GGT TCA AAA TTA AAA GAT CCT GAA CTG AGT TTA AAA GGC ACC CAG
TGT CCT AGA TCA AGT CCA AGT TTT AAT TTT CTA GGA CTT GAC TCA AAT TTT CCG TGG GTC
Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln>

      130      140      150      160      170      180
      *      *      *      *      *      *
CAC ATC ATG CAA GCA GGC CAG ACA CTG CAT CTC CAA TGC AGG GGC GAA GCA GCC CAT AAA
GTG TAG TAC GTT CGT CCG GTC TGT GAC GTA GAG GTT ACG TCC CCC CTT CGT CGG GTA TTT
His Ile Met Gln Ala Gly Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys>

      190      200      210      220      230      240
      *      *      *      *      *      *
TGG TCT TTG CCT GAA ATG GTG AGT AAG GAA AGC GAA AGG CTG AGC ATA ACT AAA TCT GCC
ACC AGA AAC GGA CTT TAC CAC TCA TTC CTT TCG CTT TCC GAC TCG TAT TGA TTT AGA CGG
Trp Ser Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys Ser Ala>

      250      260      270      280      290      300
      *      *      *      *      *      *
TGT GGA AGA AAT GGC AAA CAA TTC TGC AGT ACT TTA ACC TTG AAC ACA GCT CAA GCA AAC
ACA CCT TCT TTA CCG TTT GTT AAG ACG TCA TGA AAT TGG AAC TTG TGT CGA GTT CGT TTG
Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu Asn Thr Ala Gln Ala Asn>

      310      320      330      340      350      360
      *      *      *      *      *      *
CAC ACT GGC TTC TAC AGC TGC AAA TAT CTA GCT GTA CCT ACT TCA AAG AAG AAG GAA ACA
GTG TGA CCG AAG ATG TCG ACG TTT ATA GAT CGA CAT GGA TGA AGT TTC TTC TTC CTT TGT
His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu Ala Val Pro Thr Ser Lys Lys Lys Glu Thr>

      370      380      390      400      410      420
      *      *      *      *      *      *
GAA TCT GCA ATC TAT ATA TTT ATT AGT GAT ACA GGT AGA CCT TTC GTA GAG ATG TAC AGT
CTT AGA CGT TAG ATA TAT AAA TAA TCA CTA TGT CCA TCT GGA AAG CAT CTC TAC ATG TCA
Glu Ser Ala Ile Tyr Ile Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser>

      430      440      450      460      470      480
      *      *      *      *      *      *
GAA ATC CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT
CTT TAG GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA
Glu Ile Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys Arg Val>

      490      500      510      520      530      540
      *      *      *      *      *      *
ACG TCA CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT
TGC AGT GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA
Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu Asp Thr Leu Ile Pro Asp>

```

* * * * *

GGA AAA CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA
CCT TTT GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT
Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys>

610 620 630 640 650 660

* * * * *

GAA ATA GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT
CTT TAT CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA
Glu Ile Gly Leu Leu Thr Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr>

670 680 690 700 710 720

* * * * *

CTC ACA CAT CGA CAA ACC AAT ACA ATC ATA GAT GTC CAA ATA AGC ACA CCA CGC CCA GTC
GAG TGT GTA GCT GTT TGG TTA TGT TAG TAT CTA CAG GTT TAT TCG TGT GGT GCG GGT CAG
Leu Thr His Arg Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Ser Thr Pro Arg Pro Val>

730 740 750 760 770 780

* * * * *

AAA TTA CTT AGA GGC CAT ACT CTT GTC CTC AAT TGT ACT GCT ACC ACT CCC TTG AAC ACG
TTT AAT GAA TCT CCG GTA TGA GAA CAG GAG TTA ACA TGA CGA TGG TGA GGG AAC TTG TGC
Lys Leu Leu Arg Gly His Thr Leu Val Leu Asn Cys Thr Ala Thr Thr Pro Leu Asn Thr>

790 800 810 820 830 840

* * * * *

AGA GTT CAA ATG ACC TGG AGT TAC CCT GAT GAA AAA AAT AAG AAC GCT TCC GTA AGG CGA
TCT CAA GTT TAC TGG ACC TCA ATG GGA CTA CTT TTT TTA TTC TTG CGA AGG CAT TCC GCT
Arg Val Gln Met Thr Trp Ser Tyr Pro Asp Glu Lys Asn Lys Asn Ala Ser Val Arg Arg>

850 860 870 880 890 900

* * * * *

CGA ATT GAC CAA AGC AAT TCC CAT GCC AAC ATA TTC TAC AGT GTT CTT ACT ATT GAC AAA
GCT TAA CTG GTT TCG TTA AGG GTA CGG TTG TAT AAG ATG TCA CAA GAA TGA TAA CTG TTT
Arg Ile Asp Gln Ser Asn Ser His Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile Asp Lys>

910 920 930 940 950 960

* * * * *

ATG CAG AAC AAA GAC AAA GGA CTT TAT ACT TGT CGT GTA AGG AGT GGA CCA TCA TTC AAA
TAC GTC TTG TTT CTG TTT CCT GAA ATA TGA ACA GCA CAT TCC TCA CCT GGT AGT AAG TTT
Met Gln Asn Lys Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Ser Gly Pro Ser Phe Lys>

970 980 990 1000 1010 1020

* * * * *

TCT GTT AAC ACC TCA GTG CAT ATA TAT GAT AAA GCA GGC CCG GGC GAG CCC AAA TCT TGT
AGA CAA TTG TGG AGT CAC GTA TAT ATA CTA TTT CGT CCG GGC CCG CTC GGG TTT AGA ACA
Ser Val Asn Thr Ser Val His Ile Tyr Asp Lys Ala Gly Pro Gly Glu Pro Lys Ser Cys>

1030 1040 1050 1060 1070 1080

* * * * *

GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC
CTG TTT TGA GTG TGT ACG GGT GGC ACG GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val>

1090				1100				1110				1120				1130				1140			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	AAG	GAG	AAG	GGG
GAG	AAG	GGG	GGT	TTT	GGG	TTC	CTG	TGG	GAG	TAC	TAG	AGG	GCC	TGG	GGA	CTC	CAG	TGT		Phe	Leu	Phe	Pro
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr>				
1150				1160				1170				1180				1190				1200			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	ACG	CAC	CAC	CAC
CTG	CAC	CAC	CTG	CAC	TCG	GTG	CTT	CTG	GGA	CTC	CAG	TTC	AAG	TTG	ACC	ATG	CAC	CTG		Cys	Val	Val	Val
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp>				
1210				1220				1230				1240				1250				1260			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CCG	CAC	CTC	CAC
CTC	CAC	CTC	CAC	GTA	TTA	CGG	TTC	TGT	TTC	GGC	GCC	CTC	CTC	GTC	ATG	TTG	TCG	TGC	ATG	Gly	Val	Glu	Val
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr>				
1270				1280				1290				1300				1310				1320			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	GCA	CAC	CAG	TCG
CTC	CAG	TCG	CAG	GAG	TGG	CAG	GAC	GTG	GTC	CTG	ACC	GAC	TTA	CCG	TTC	CTC	ATG	TTC		Arg	Val	Val	Ser
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys>				
1330				1340				1350				1360				1370				1380			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
TGC	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	ACG	TTC	CAG	AGG
CTC	TTC	CAG	AGG	TTG	TTT	CGG	GAG	GGT	CGG	GGG	TAG	CTC	TTT	TGG	TAG	AGG	TTT	CGG	TTT	Cys	Lys	Val	Ser
Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys>				
1390				1400				1410				1420				1430				1440			
*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG	CCC	GTC	GGG	GCT
CTC	GTC	GGG	GCT	CTT	GGT	GTC	CAC	ATG	TGG	GAC	GGG	GGT	AGG	GCC	CTA	CTC	GAC	TGG	TTC	Gly	Gln	Pro	Arg
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys>				
14																							

Figure 16D

```

      1630      1640      1650      1660      1670      1680
      *      *      *      *      *      *      *
AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC
TTG CAG AAG AGT ACG AGG CAC TAC GTA CTC CGA GAC GTG TTG GTG ATG TGC GTC TTC TCG
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser>

      1690      1700
      *      *      *      *
CTC TCC CTG TCT CCG GGT AAA TGA
GAG AGG GAC AGA GGC CCA TTT ACT
Leu Ser Leu Ser Pro Gly Lys ***>

```

097387.013401
 101210 2282250

Figure 17

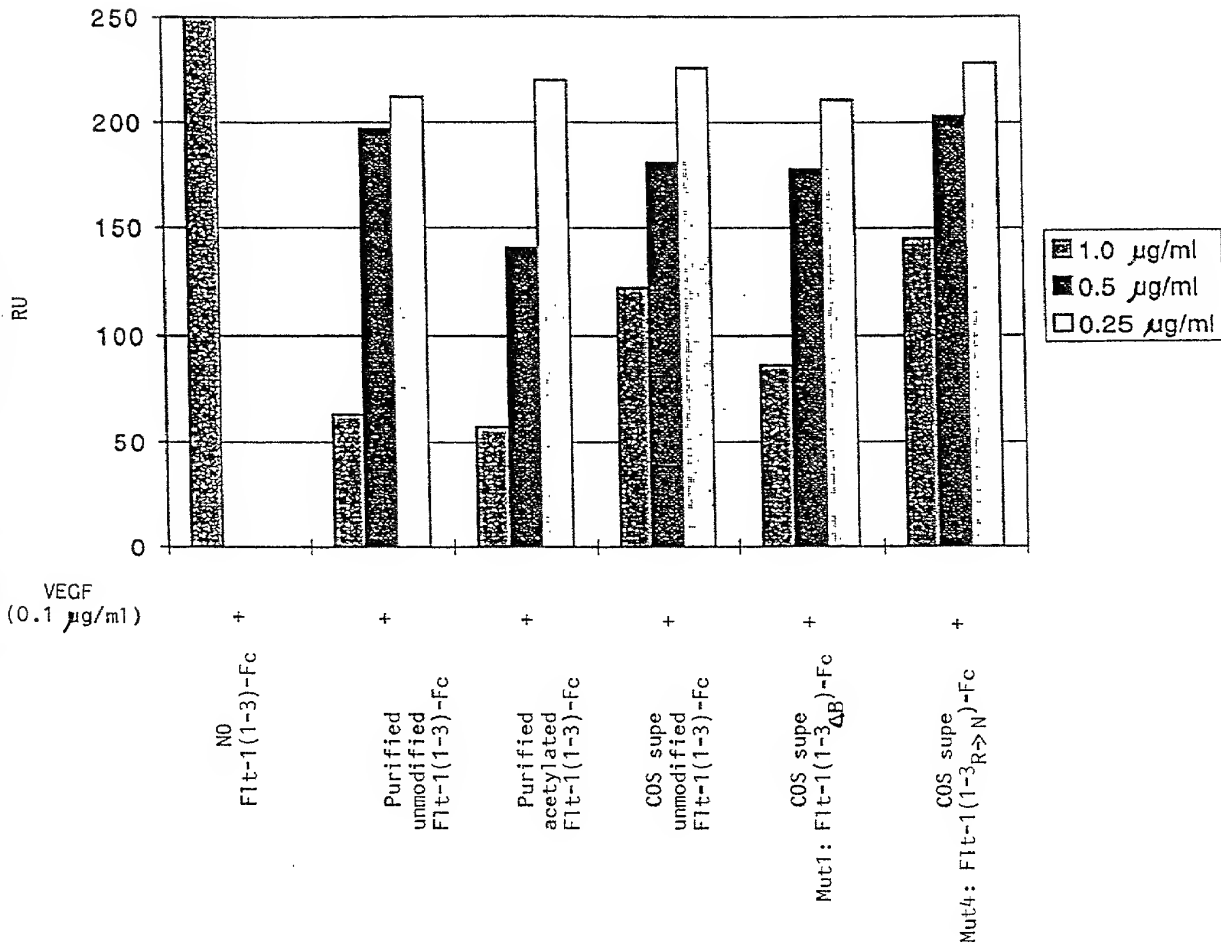


Figure 18

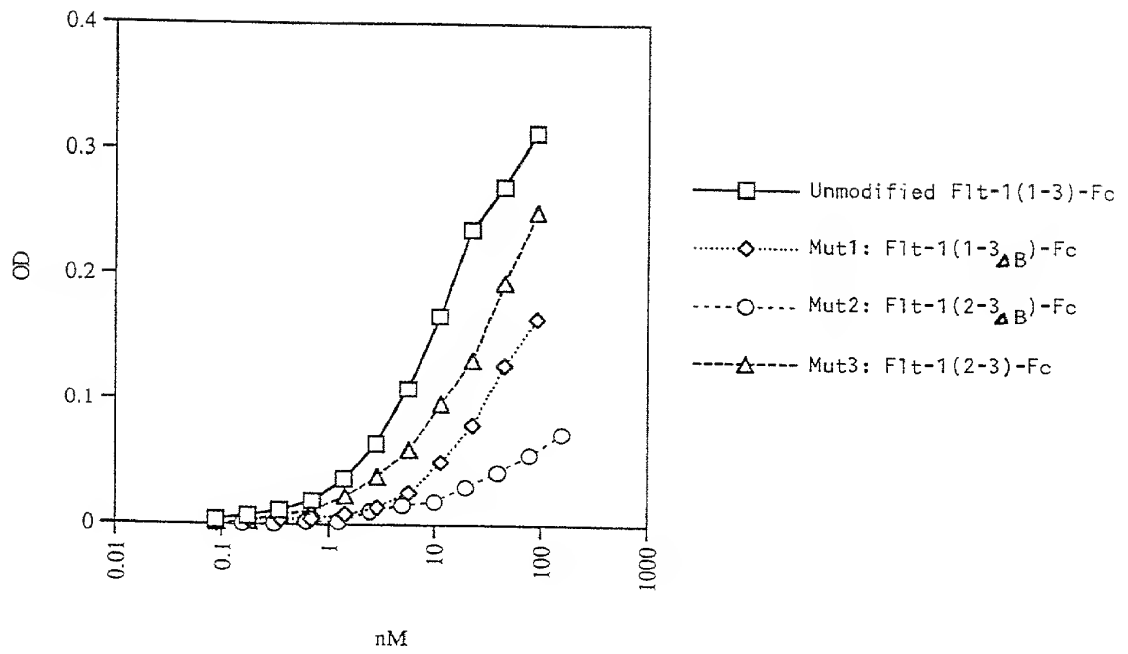


Figure 19

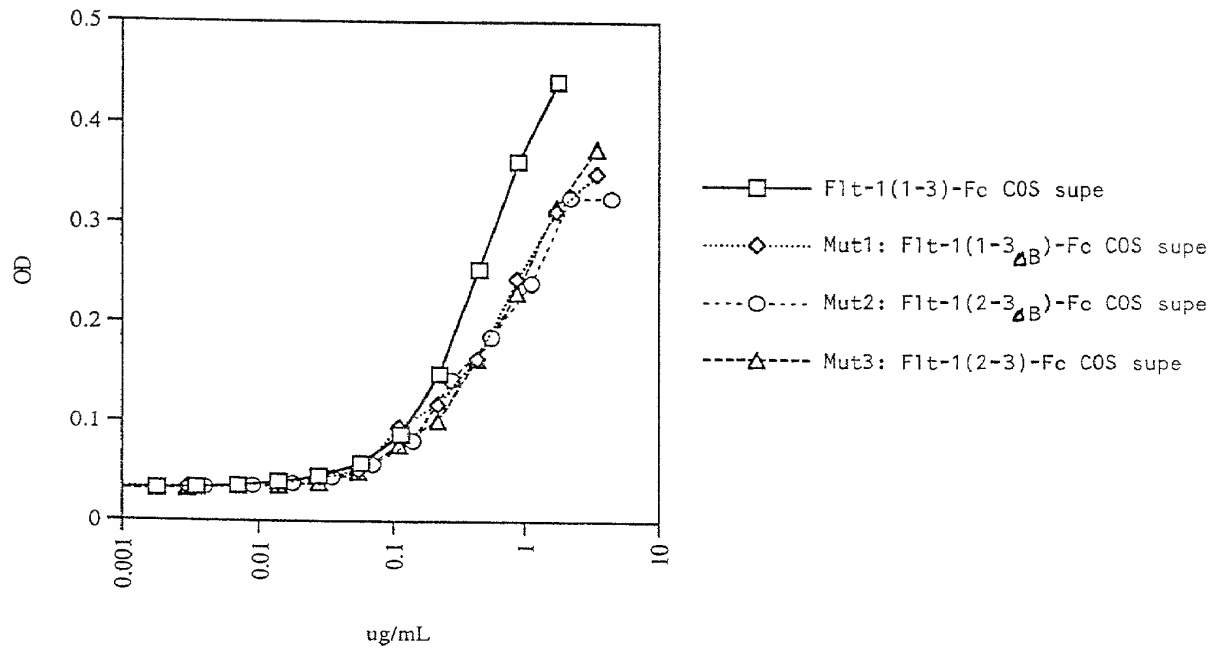


Figure 20

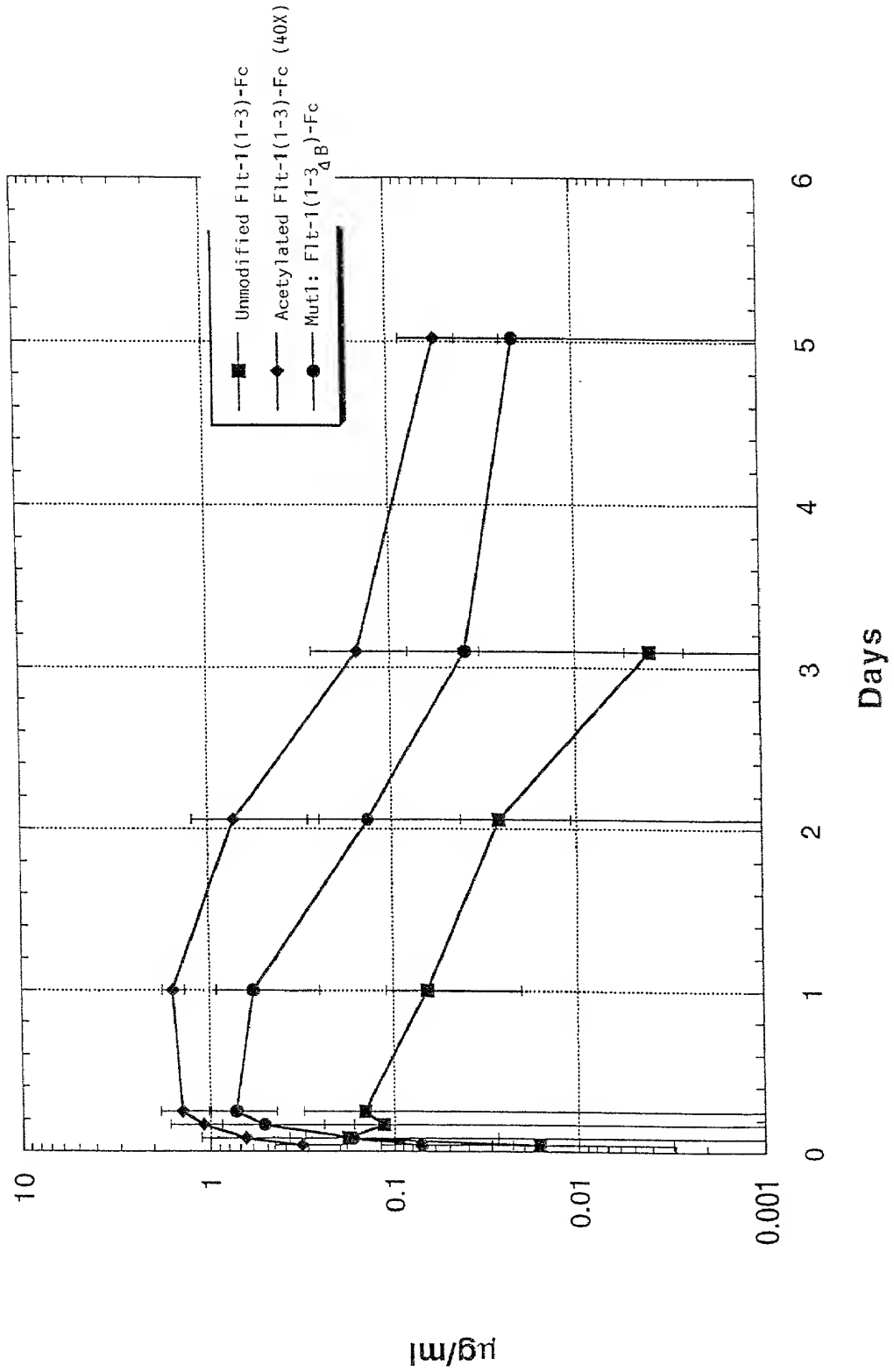


Figure 21A

```

                                >EcoRI_site
                                |
      10      20      30      40      50      60      70      80
AAGCTTGGGCTGCAGGTCGATCGACTCTAGAGGATCGATCCCGGGCGAGCTCGAATTCGCAACCACCATGGTCAGCTAC
TTCGAACCCGACGTCACAGCTAGCTGAGATCTCCTAGCTAGGGGCCCGCTCGAGCTTAAGCGTTGGTGGTACCAGTCGATG
                                M V S Y>
                                1      4
                                _____>

                                >BspEI_bridge
                                |
      90      100      110      120      130      140      150      160
TGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTCAGGATCTAGTTCGGGAGGTAGACCTTTCGT
ACCCTGTGTGCCCCAGGACGACACGCGCGACGAGTGCAGACGAAGAGTGTCTAGATCAAGGCCTCCATCTGGAAGCA
W D T G V L L C A L L S C L L L T G S S>
_____FLT1 SS_____>
                                S G>
                                _____>
                                G R P F V>
                                31
                                _____>

      170      180      190      200      210      220      230      240
AGAGATGTACAGTGAAATCCCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTTCATTCCTGCCGGGTTACGTCAC
TCTCTACATGTCACTTTAGGGGCTTTAATATGTGTACTGACTTCCTTCCTCGAGCAGTAAGGGACGGCCCAATGCAGTG
E M Y S E I P E I I H M T E G R E L V I P C R V T S>
                                57
_____HFLT1 D2_____>

      250      260      270      280      290      300      310      320
CTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAACACGCATAATCTGGGACAGTAGA
GATTGTAGTGACAATGAAATTTTTTCAAAGGTGAAGTGTGAAACTAGGGACTACCTTTTGGCGTATTAGACCTGTCACTCT
P N I T V T L K K F P L D T L I P D G K R I I W D S R>
                                84
_____HFLT1 D2_____>

      330      340      350      360      370      380      390      400
AAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTGTGA
TTCCCGAAGTAGTATAGTTTACGTTGCATGTTTCTTTATCCCGAAGACTGGACACTTCGTTGTGAGTTACCCGTAAACAT
K G F I I S N A T Y K E I G L L T C E A T V N G H L Y>
                                111
_____HFLT1 D2_____>

      410      420      430      440      450      460      470      480
TAAGACAACTATCTCACACATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGCTCTCATGGAATTGAACTAT
ATTCTGTTTGTAGAGTGTGTAGCTGTTTGGTTATGTTAGTATCTACACCAAGACTCAGGCAGAGTACCTTAACCTTGATA
K T N Y L T H R Q T N T I I D>
_____HFLT1 D2_____>
                                V V L S P S H G I E L>
                                137
_____HFLK1 D3_____>

```

Figure 21B

```

      490      500      510      520      530      540      550      560
CTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAAGCTGAACATAATGTGGGGATTGACTTCAACTGGGAATACCCCT
GACAACCTCTTTTCGAACAGAAATTTAACATGTCGTTCTTGACTTGATTTACACCCCTAACTGAAGTTGACCCCTATGGGA
S V G E K L V L N C T A R T E L N V G I D F N W E Y P>
                                                                164
_____HFLK1 D3_____>

      570      580      590      600      610      620      630      640
TCTTCGAAGCATCAGCATAAGAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGAG
AGAAGCTTCGTAGTCGTATCTTTGAACATTTGGCTCTGGATTTTTGGGTGACACCCCTCACTCTACTCTTTTAAAACTC
S S K H Q H K K L V N R D L K T Q S G S E M K K F L S>
                                                                191
_____HFLK1 D3_____>

      650      660      670      680      690      700      710      720
CACCTTAACTATAGATGGTGTAAACCGGAGTGACCAAGGATTCGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGA
GTGGAATTGATACTACACATTTGGCCCTCACTGGTTCCTAACATGTGGACACGTCGTAGGTACCCGACTACTGGTTCT
T L T I D G V T R S D Q G L Y T C A A S S G L M T K>
                                                                217
_____HFLK1 D3_____>

      >Srf_Bridge_
      |
      730      740      750      760      770      780      790      800
AGAACAGCACATTTGTTCAGGGTCCATGAAAAGGGCCCGGGCGACAAACTCACACATGCCACCGTGCCAGCACCTGAA
TCTTGTCGTGTAAACAGTCCCAGTACTTTTCCCGGGCCCGCTGTTTGTAGTGTGTACGGGTGGCACGGGTGCTGGACTT
K N S T F V R V H E K>
_____HFLK1 D3_____>
      G P G>
      _____>
      D K T H T C P P C P A P E>
                                                                244
_____FCΔC1 (A)_____>

      810      820      830      840      850      860      870      880
CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTAC
GAGGACCCCTTGGCAGTCAGAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTG
L L G G P S V F L F P P K P K D T L M I S R T P E V T>
                                                                271
_____FCΔC1 (A)_____>

      890      900      910      920      930      940      950      960
ATGCGTGGTGGTGAGCGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATG
TACGCACCCACCTGCCTCGGTGCTTCTGGGACTCCAGTTCAGTTGACCATGCACCTGCCGCACCTCCACGTATTAC
C V V V D V S H E D P E V K F N W Y V D G V E V H N>
                                                                297
_____FCΔC1 (A)_____>

      970      980      990      1000      1010      1020      1030      1040
CCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCCCTACCCGTCTGCACCAGGACTGG
GGTTCGTGTTTCGGCGCCCTCCTCGTCATGTGTGTCGTCATGGCACACCCAGTCCGAGGAGTGGCAGGACGTGGTCTGACC
A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W>
                                                                324
_____FCΔC1 (A)_____>

```

1050 1060 1070 1080 1090 1100 1110 1120
CTGAATGGCAAGGAGTACAAGTGC AAGGTC TCCAA CAAAGCCCTCCAGACCCCCATCGAGAAAACCATCTCCAAAGCCAA
GACTTACCGTTCTCTCATGTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT
L N G K E Y K C K V S N K A L P A P I E K T I S K A >
FCAC (A) >

```

                                     >A>C_A_allotype
                                     |
                                     >G>T_A_allotype
                                     |
1130      1140      1150      1160      1170      |      1180      1190      1200
AGGGCAGCCCCGAGAAACCACAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCCAGGTCAGCCTGACCT
TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTCGGA
  G  Q  P  R  E  P  Q  V  Y  T  L  P  P  S  R  D  E  L  T  K  N  Q  V  S  L  T>
                                     FCAC1 (A)
                                     377

```

1210 1220 1230 1240 1250 1260 1270 1280
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACC
CGGACCAGTTTCCGAAGATAGGGTCGCTGTATGCGGCACCTCACCCTCTCGTTACCCGTCGGCCCTCTGTTGATGTTCTGG
C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T>
FCAC1 (A)

```

                                     >T>C
                                     |
1290      1300      1310      1320      1330      1340      1350      1360
ACGCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG
TGGCGAGGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATATCGTTCGAGTGGCACCTGTTCTCGTCCACCCTCGTCCCC
T P P V L D S D G S F F L Y S K L T V D K S R W Q Q G>
                                     431
                                     FCAC1 (A)
                                     >

```

1370 1380 1390 1400 1410 1420 1430 1440
GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTA
CTTGCAGAAGAGTACGAGGCACTACGTA CTCCGAGACGTGTTGGTGATGTGCGCTCTTCTCGGAGAGGGACAGAGGCCCAT
N V F S C S V M H E A L H N H Y T Q K S L S L S P G>
457
FCAC1 (A)

```

>NotI_site
      |
      |1450
AATGAGCGGCCGC
T TACTCGCCGGCG
K  *>
458
      >

```

Figure 22A

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>EcoRI_site
```

Figure 22B

490 500 510 520 530 540 550 560
 TGGTAGGGGAGAAGCTGGTCCTCAACTGCACCGTGTGGGCTGAGTTTAACTCAGGTGTCACCTTTGACTGGGACTACCCA
 ACCATCCCCCTCTTCGACCAGGAGTTGACGTGGCACACCCGACTCAAATGAGTCCACAGTGGAAACTGACCCTGATGGGT
 L V G E K L V L N C T V W A E F N S G V T F D W D Y P>
 164
 _____VEGFR3 (FLT4) IG DOMAIN 3_____>

570 580 590 600 610 620 630 640
 GGGAAAGCAGGCAGAGCGGGTAAGTGGGTGCCCGAGCGACGCTCCCAACAGACCCACACAGAAGTCTCCAGCATCCTGAC
 CCCTTCGTCCGTCTCGCCCCCAFTCACCCACGGGCTCGCTGCGAGGGTTGTCTGGGTGTGCTTTGAGAGGTCGTAGGACTG
 G K Q A E R G K W V P E R R S Q Q T H T E L S S I L T>
 191
 _____VEGFR3 (FLT4) IG DOMAIN 3_____>

650 660 670 680 690 700 710 720
 CATCCACAACGTCAGCCAGCACGACCTGGGCTCGTATGTGTGCAAGGCCAACACGGCATCCAGCGATTTCGGGAGAGCA
 GTAGTGTTCAGTCGGTCTGCTGGACCCGAGCATAACACAGTTCCGGTGTGTTGCGGTAGTTCGCTAAAGCCCTCTCGT
 I H N V S Q H D L G S Y V C K A N N G I Q R F R E S>
 217
 _____VEGFR3 (FLT4) IG DOMAIN 3_____>

730 740 750 760 770 780 790 800
 CCGAGGTCATTGTGCATGAAATGGCCCCGGGCGACAAACTCACACATGCCACCGTGCCAGCACCTGAAGTCTCTGGG
 GGCTCCAGTAACACGTACTTTTACCGGGCCCGCTGTTTTGAGTGTGTACGGGTGGCACGGGTCTGGAAGTTCGAGGACCC
 T E V I V H E N>
 _____VEGFR3 (FLT4) IG_____>
 G P G>
 _____>
 D K T H T C P P C P A P E L L G>
 244
 _____FCAC1 - A ALLOTYP_____>

810 820 830 840 850 860 870 880
 GGACCGTCAGTCTTCCTCTTCCCCCAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTGACATGCGTGGT
 CCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCCTGGGGACTCCAGTGTACGCACCA
 G P S V F L F P P K P K D T L M I S R T P E V T C V V>
 271
 _____FCAC1 - A ALLOTYP_____>

890 900 910 920 930 940 950 960
 GGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA
 CCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTT
 V D V S H E D P E V K F N W Y V D G V E V H N A K T>
 297
 _____FCAC1 - A ALLOTYP_____>

970 980 990 1000 1010 1020 1030 1040
 AGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCTCCACCGTCTGCACCAGGACTGGCTGAATGGC
 TCGGCGCCCTCCTCGTCATGTTGTGCTGCATGGCACACCAAGTCCGAGGAGTGGCAGGACGTGGTCTTGACCGACTTACCG
 K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G>
 324
 _____FCAC1 - A ALLOTYP_____>

```

1050      1060      1070      1080      1090      1100      1110      1120
AAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCC
TTCCTCATGTTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG
K E Y K C K V S N K A L P A P I E K T I S K A K G Q P>
                                                                351
_____FCAC1 - A ALLOTYP E_____>

                                >A>C_A_allotype
                                |
                                >G>T_A_allotype
                                |
                                |
1130      1140      1150      1160      1170      1180      1190      1200
CCGGAACCCACAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCGTGGTCA
GGCTCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGGTTCCTTGGTCCAGTCGGACTGGACGGACCACT
R E P Q V Y T L P P S R D E L T K N Q V S L T C L V>
                                                                377
_____FCAC1 - A ALLOTYP E_____>

1210      1220      1230      1240      1250      1260      1270      1280
AAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCCGAGAAACAACCTACAAGACCACGCTCCC
TTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTCTGTGATGTTCTGGTTCGGAGGG
K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P>
                                                                404
_____FCAC1 - A ALLOTYP E_____>

                                >T>C
                                |
1290      1300      1310      1320      1330      1340      1350      1360
GTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTT
CACGACCTGAGGCTGCCGAGGAAGAAGGAGATATCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCTTGCAGAA
V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F>
                                                                431
_____FCAC1 - A ALLOTYP E_____>

                                                                >NotI_site
                                                                |
1370      1380      1390      1400      1410      1420      1430      1440
CTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGACCTCTCCCTGTCTCCGGGTAAATGAGCGG
GAGTACGAGGCACTACGTACTCCGAGACGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTACTCGCC
S C S V M H E A L H N H Y T Q K S L S L S P G K *>
                                                                455
_____FCAC1 - A ALLOTYP E_____>

CCGC
GGCG

```

Figure 23

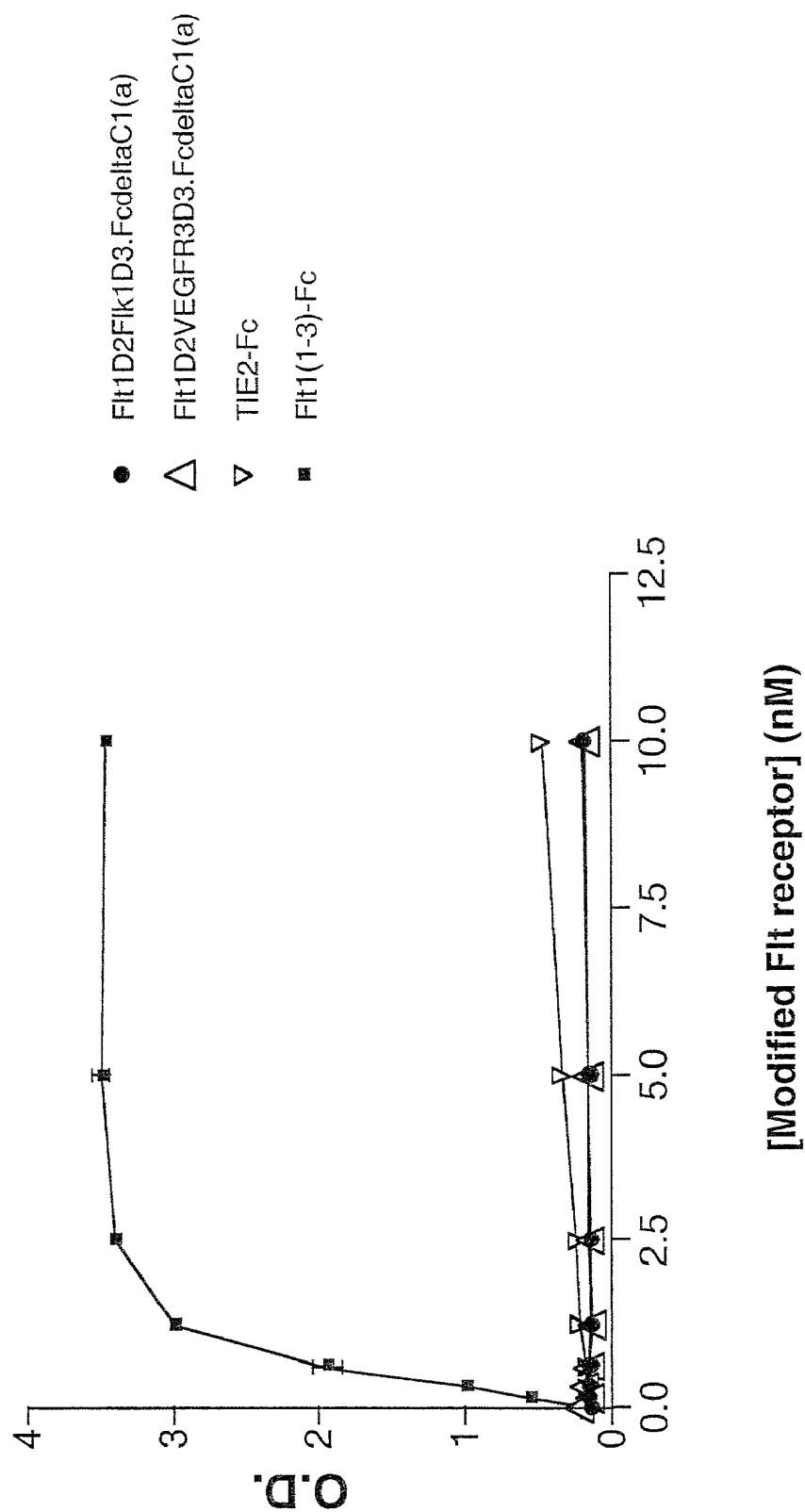


Figure 24A

10 20 30 40 50 60
 * * * * * *
 ATG GTC AGC TAC TGG GAC ACC GGG GTC CTG CTG TGC GCG CTG CTC AGC TGT CTG CTT CTC
 TAC CAG TCG ATG ACC CTG TGG CCC CAG GAC GAC ACG CGC GAC GAG TCG ACA GAC GAA GAG
 M V S Y W D T G V L L C A L L S C L L L>
 1_____5_____hFLT1 SIGNAL SEQUENCE_____15_____20>

70 80 90 100 110 120
 * * * * * *
 ACA GGA TCT AGT TCC GGA AGT GAT ACC GGT AGA CCT TTC GTA GAG ATG TAC AGT GAA ATC
 TGT CCT AGA TCA AGG CCT TCA CTA TGG CCA TCT GGA AAG CAT CTC TAC ATG TCA CTT TAG
 T G S S S G>
 21_hFLT1 SIGNAL SEQ_26>

 S D T G R P F V E M Y S E I>
 27_____30_____hFLT1 IG DOMAIN 2_____40>

130 140 150 160 170 180
 * * * * * *
 CCC GAA ATT ATA CAC ATG ACT GAA GGA AGG GAG CTC GTC ATT CCC TGC CGG GTT ACG TCA
 GGG CTT TAA TAT GTG TAC TGA CTT CCT TCC CTC GAG CAG TAA GGG ACG GCC CAA TGC AGT
 P E I I H M T E G R E L V I P C R V T S>
 41_____45_____hFLT1 IG DOMAIN 2_____55_____60>

190 200 210 220 230 240
 * * * * * *
 CCT AAC ATC ACT GTT ACT TTA AAA AAG TTT CCA CTT GAC ACT TTG ATC CCT GAT GGA AAA
 GGA TTG TAG TGA CAA TGA AAT TTT TTC AAA GGT GAA CTG TGA AAC TAG GGA CTA CCT TTT
 P N I T V T L K K F P L D T L I P D G K>
 61_____65_____hFLT1 IG DOMAIN 2_____75_____80>

250 260 270 280 290 300
 * * * * * *
 CGC ATA ATC TGG GAC AGT AGA AAG GGC TTC ATC ATA TCA AAT GCA ACG TAC AAA GAA ATA
 GCG TAT TAG ACC CTG TCA TCT TTC CCG AAG TAG TAT AGT TTA CGT TGC ATG TTT CTT TAT
 R I I W D S R K G F I I S N A T Y K E I>
 81_____85_____hFLT1 IG DOMAIN 2_____95_____100>

310 320 330 340 350 360
 * * * * * *
 GGG CTT CTG ACC TGT GAA GCA ACA GTC AAT GGG CAT TTG TAT AAG ACA AAC TAT CTC ACA
 CCC GAA GAC TGG ACA CTT CGT TGT CAG TTA CCC GTA AAC ATA TTC TGT TTG ATA GAG TGT
 G L L T C E A T V N G H L Y K T N Y L T>
 101_____105_____hFLT1 IG DOMAIN 2_____115_____120>

370 380 390 400 410 420
 * * * * * *
 CAT CGA CAA ACC AAT ACA ATC ATA GAT GTG GTT CTG AGT CCG TCT CAT GGA ATT GAA CTA
 GTA GCT GTT TGG TTA TGT TAG TAT CTA CAC CAA GAC TCA GGC AGA GTA CCT TAA CTT GAT
 H R Q T N T I I D>
 121_____hFLT1 IG DOMAIN 2_____129>

 V V L S P S H G I E L>
 130_____hFLK1 IG DOMAIN 3_____140>

```

      430      440      450      460      470      480
      *        *        *        *        *        *
TCT GTT GGA GAA AAG CTT GTC TTA AAT TGT ACA GCA AGA ACT GAA CTA AAT GTG GGG ATT
AGA CAA CCT CTT TTC GAA CAG AAT TTA ACA TGT CGT TCT TGA CTT GAT TTA CAC CCC TAA
S   V   G   E   K   L   V   L   N   C   T   A   R   T   E   L   N   V   G   I>
141_____145_____hFLK1 IG DOMAIN 3_____155_____160>

      490      500      510      520      530      540
      *        *        *        *        *        *
GAC TTC AAC TGG GAA TAC CCT TCT TCG AAG CAT CAG CAT AAG AAA CTT GTA AAC CGA GAC
CTG AAG TTG ACC CTT ATG GGA AGA AGC TTC GTA GTC GTA TTC TTT GAA CAT TTG GCT CTG
D   F   N   W   E   Y   P   S   S   K   H   Q   H   K   K   L   V   N   R   D>
161_____165_____hFLK1 IG DOMAIN 3_____175_____180>

      550      560      570      580      590      600
      *        *        *        *        *        *
CTA AAA ACC CAG TCT GGG AGT GAG ATG AAG AAA TTT TTG AGC ACC TTA ACT ATA GAT GGT
GAT TTT TGG GTC AGA CCC TCA CTC TAC TTC TTT AAA AAC TCG TGG AAT TGA TAT CTA CCA
L   K   T   Q   S   G   S   E   M   K   K   F   L   S   T   L   T   I   D   G>
181_____185_____hFLK1 IG DOMAIN 3_____195_____200>

      610      620      630      640      650      660
      *        *        *        *        *        *
GTA ACC CGG AGT GAC CAA GGA TTG TAC ACC TGT GCA GCA TCC AGT GGG CTG ATG ACC AAG
CAT TGG GCC TCA CTG GTT CCT AAC ATG TGG ACA CGT CGT AGG TCA CCC GAC TAC TGG TTC
V   T   R   S   D   Q   G   L   Y   T   C   A   A   S   S   G   L   M   T   K>
201_____205_____hFLK1 IG DOMAIN 3_____215_____220>

      670      680      690      700      710      720
      *        *        *        *        *        *
AAG AAC AGC ACA TTT GTC AGG GTC CAT GAA AAG GAC AAA ACT CAC ACA TGC CCA CCG TGC
TTC TTG TCG TGT AAA CAG TCC CAG GTA CTT TTC CTG TTT TGA GTG TGT ACG GGT GGC ACG
K   N   S   T   F   V   R   V   H   E   K>
221_____hFLK1 IG DOMAIN 3_____231>

      D   K   T   H   T   C   P   P   C>
232_____hFCAC1 A _____240>

      730      740      750      760      770      780
      *        *        *        *        *        *
CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC
GGT CGT GGA CTT GAG GAC CCC CCT GGC AGT CAG AAG GAG AAG GGG GGT TTT GGG TTC CTG
P   A   P   E   L   L   G   G   P   S   V   F   L   F   P   P   K   P   K   D>
241_____245_____hFCAC1 A _____255_____260>

      790      800      810      820      830      840
      *        *        *        *        *        *
ACC CTC ATG ATC TCC OGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA
TGG GAG TAC TAG AGG GCC TGG GGA CTC CAG TGT ACG CAC CAC CAC CTG CAC TCG GTG CTT
T   L   M   I   S   R   T   P   E   V   T   C   V   V   V   D   V   S   H   E>
261_____265_____hFCAC1 A _____275_____280>

      850      860      870      880      890      900
      *        *        *        *        *        *
GAC OCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA
CTG GGA CTC CAG TTC AAG TTG ACC ATG CAC CTG CCG CAC CTC CAC CAT TTA CCG TTC TGT
D   P   E   V   K   F   N   W   Y   V   D   G   V   E   V   H   N   A   K   T>
281_____285_____hFCAC1 A _____295_____300>

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910					920					930					940					950					960				
*					*					*					*					*									
AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG										
TTC	GGC	GCC	CTC	CTC	GTC	ATG	TTG	TCG	TGC	ATG	GCA	CAC	CAG	TCG	CAG	GAG	TGG	CAG	GAC										
K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S	V	L	T	V	L										
301					305					hFCAC1 A					315					320>									
970					980					990					1000					1010					1020				
*					*					*					*					*									
CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCC	CTC	CCA										
GTG	GTC	CTG	ACC	GAC	TTA	CCG	TTC	CTC	ATG	TTC	ACG	TTC	CAG	AGG	TTG	TTT	CGG	GAG	GGT										
H	Q	D	W	L	N	G	K	E	Y	K	C	K	V	S	N	K	A	L	P										
321					325					hFCAC1 A					335					340>									
1030					1040					1050					1060					1070					1080				
*					*					*					*					*									
GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC										
CGG	GGG	TAG	CTC	TTT	TGG	TAG	AGG	TTT	CGG	TTT	CCC	GTC	GGG	GCT	CTT	GGT	GTC	CAC	ATG										
A	P	I	E	K	T	I	S	K	A	K	G	Q	P	R	E	P	Q	V	Y										
341					345					hFCAC1 A					355					360>									
1090					1100					1110					1120					1130					1140				
*					*					*					*					*									
ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC										
TGG	GAC	GGG	GGT	AGG	GCC	CTA	CTC	GAC	TGG	TTC	TTG	GTC	CAG	TCG	GAC	TGG	ACG	GAC	CAG										
T	L	P	P	S	R	D	E	L	T	K	N	Q	V	S	L	T	C	L	V										
361					365					hFCAC1 A					375					380>									
1150					1160					1170					1180					1190					1200				
*					*					*					*					*									
AAA	GGC	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC										
TTT	CCG	AAG	ATA	GGG	TCG	CTG	TAG	CGG	CAC	CTC	ACC	CTC	TCG	TTA	CCC	GTC	GGC	CTC	TTG										
K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	Q	P	E	N										
381					385					hFCAC1 A					395					400>									
1210					1220					1230					1240					1250					1260				
*					*					*					*					*									
AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG										
TTG	ATG	TTC	TGG	TGC	GGA	GGG	CAC	GAC	CTG	AGG	CTG	CCG	AGG	AAG	AAG	GAG	ATG	TCG	TTC										
N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K										
401					405					hFCAC1 A					415					420>									
1270					1280					1290					1300					1310					1320				
*					*					*					*					*									
CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT										
GAG	TGG	CAC	CTG	TTC	TCG	TCC	ACC	GTC	GTC	CCC	TTG	CAG	AAG	AGT	ACG	AGG	CAC	TAC	GTA										
L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H										

Figure 25A

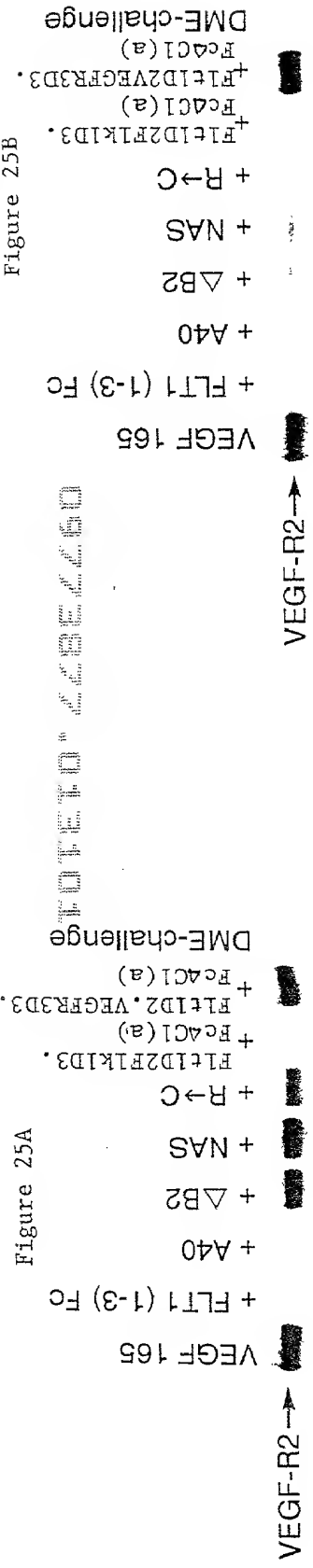


Figure 25B

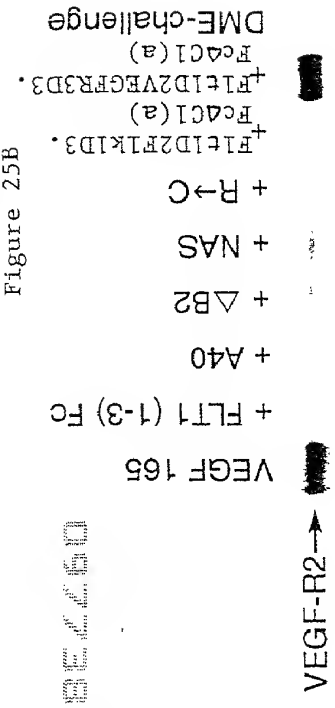
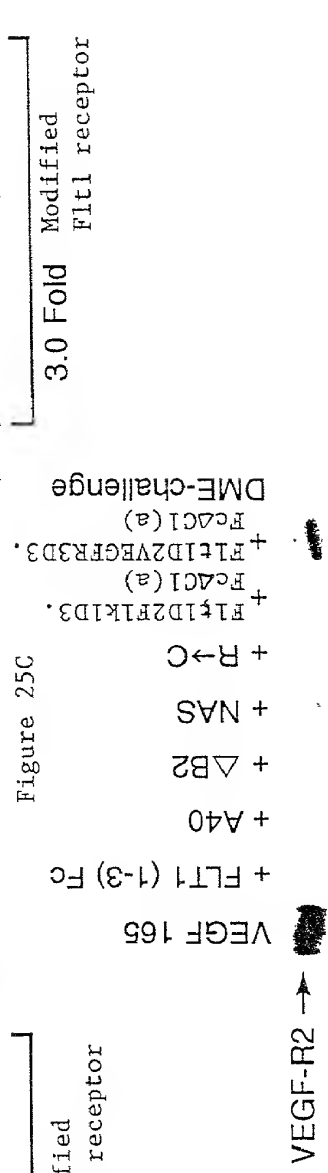


Figure 25C



1.5 Fold Modified
Flt1 receptor

3.0 Fold Modified
Flt1 receptor

6.0 Fold Modified
Flt1 receptor

Figure 27

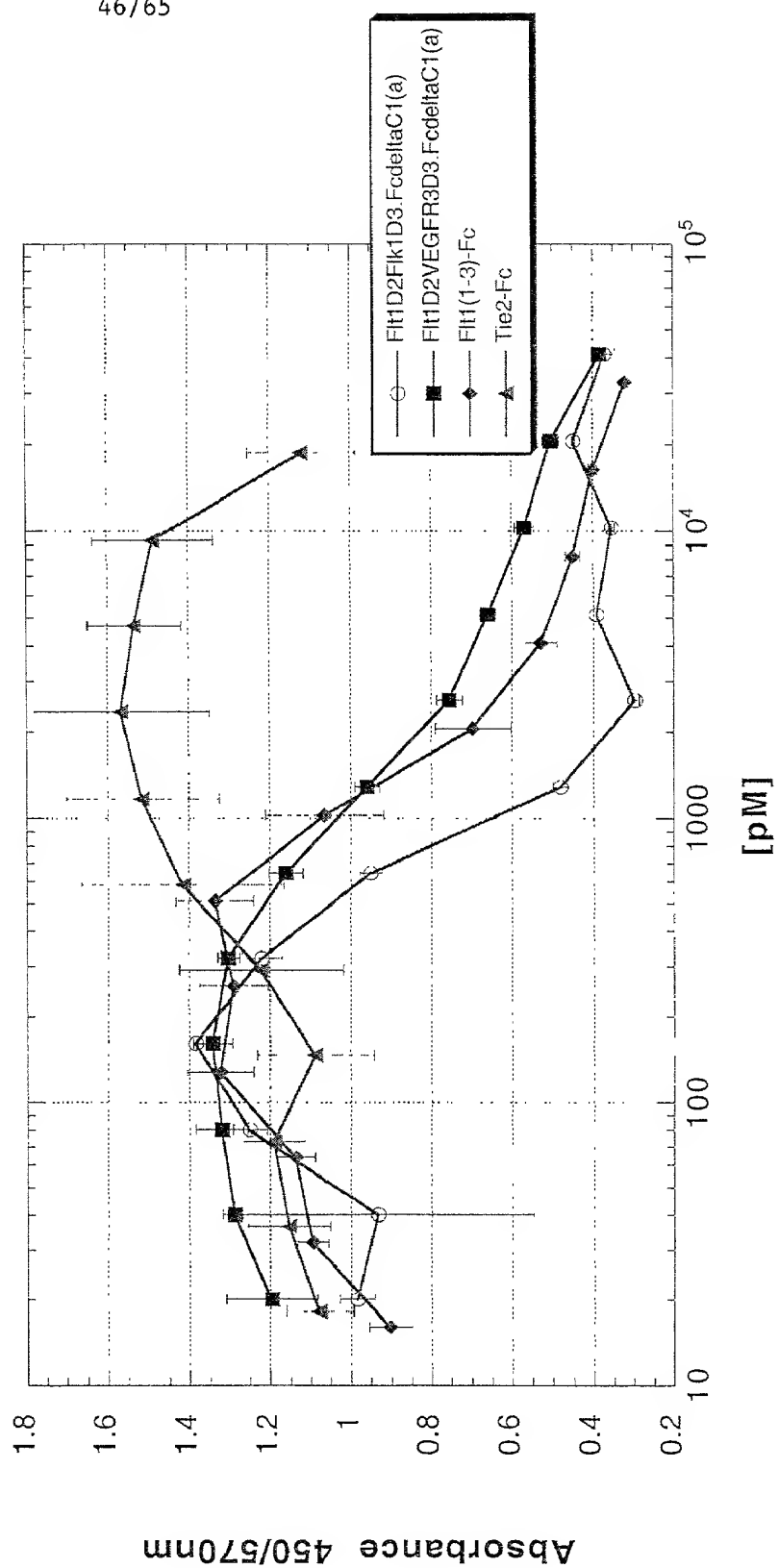


Figure 28

Binding Stoichiometry of hVEGF165 to F1t1D2F1k1D3.FcΔC1 (a) & VEGFR1R2-FcΔC1 (a)		
hVEGF165 (nM)	VEGF/F1t1D2F1k1D3.FcΔC1 (a)	VEGF/VEGFR1R2-FcΔC1 (a)
1	0.93	0.98
10	0.97	0.94
50	1	0.99
Average±StDev	0.96±0.03	0.97±0.02

Figure 29

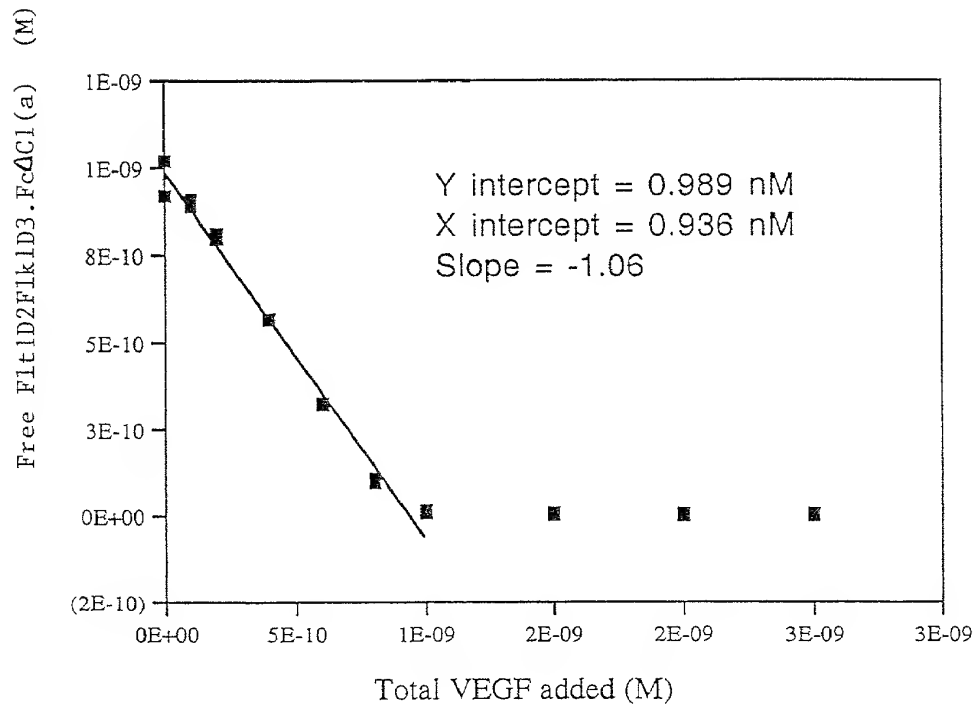


Figure 30

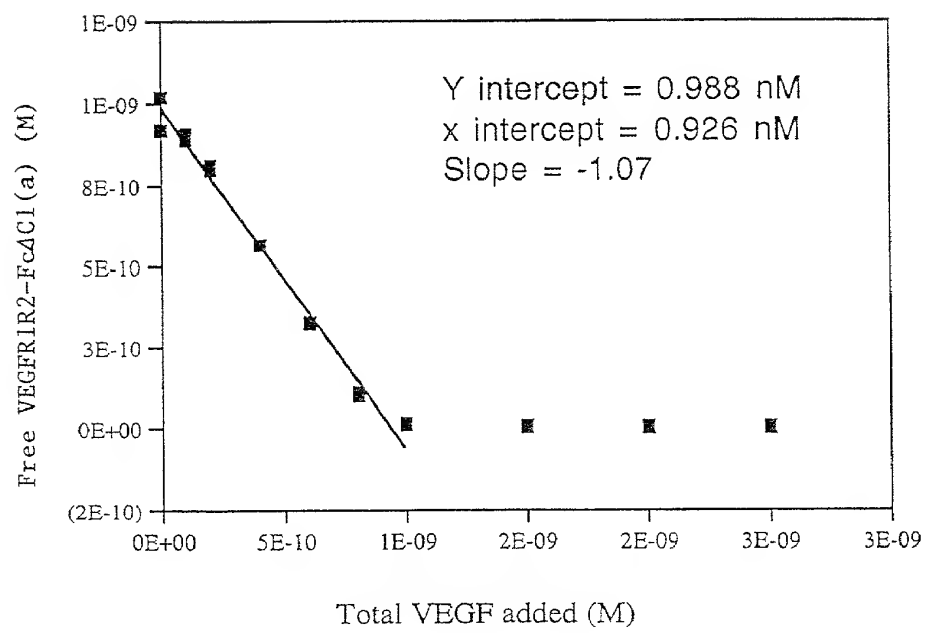


Figure 31

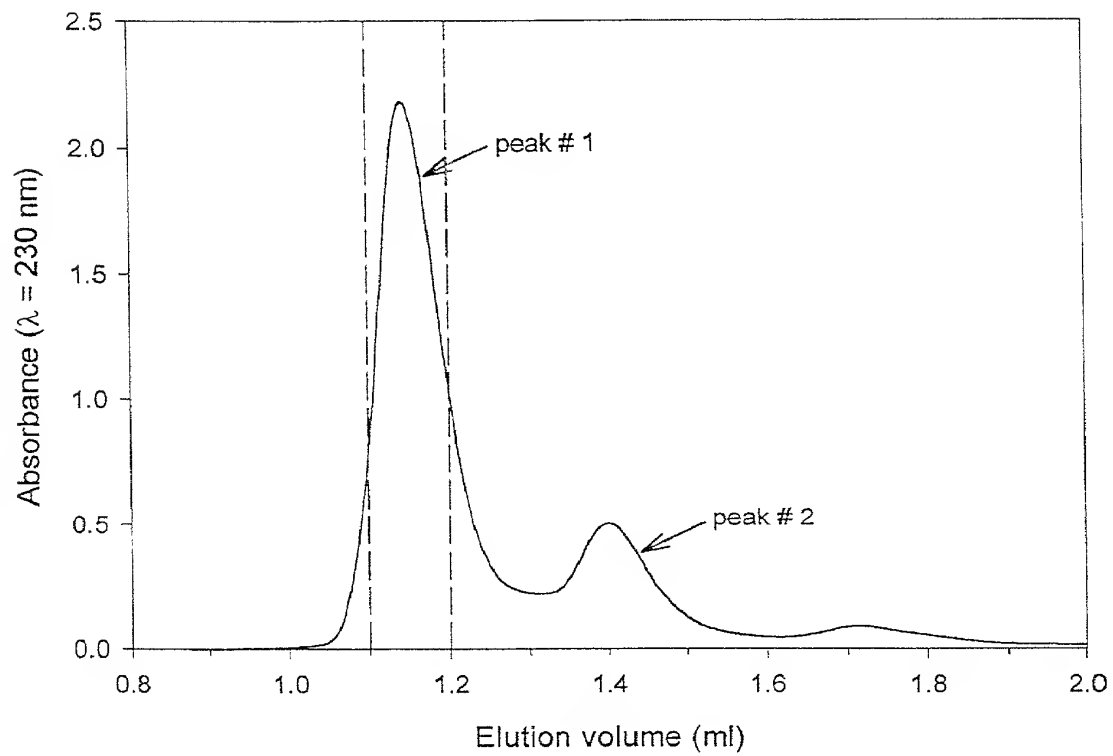


Figure 32

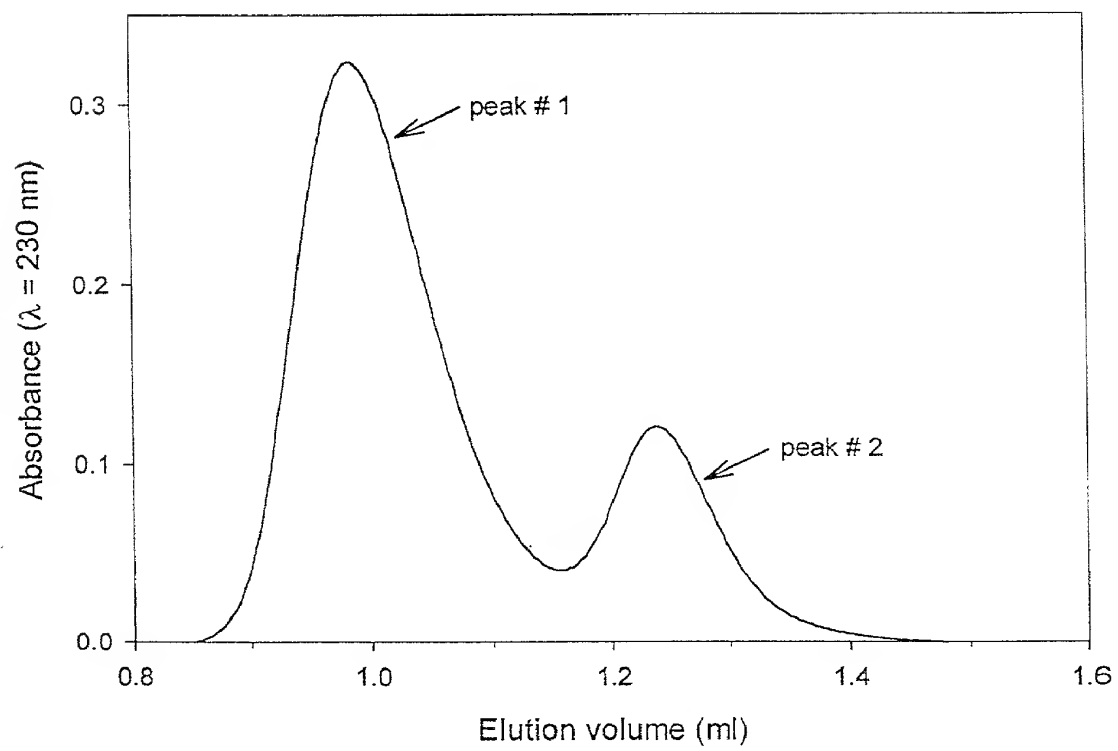


Figure 33

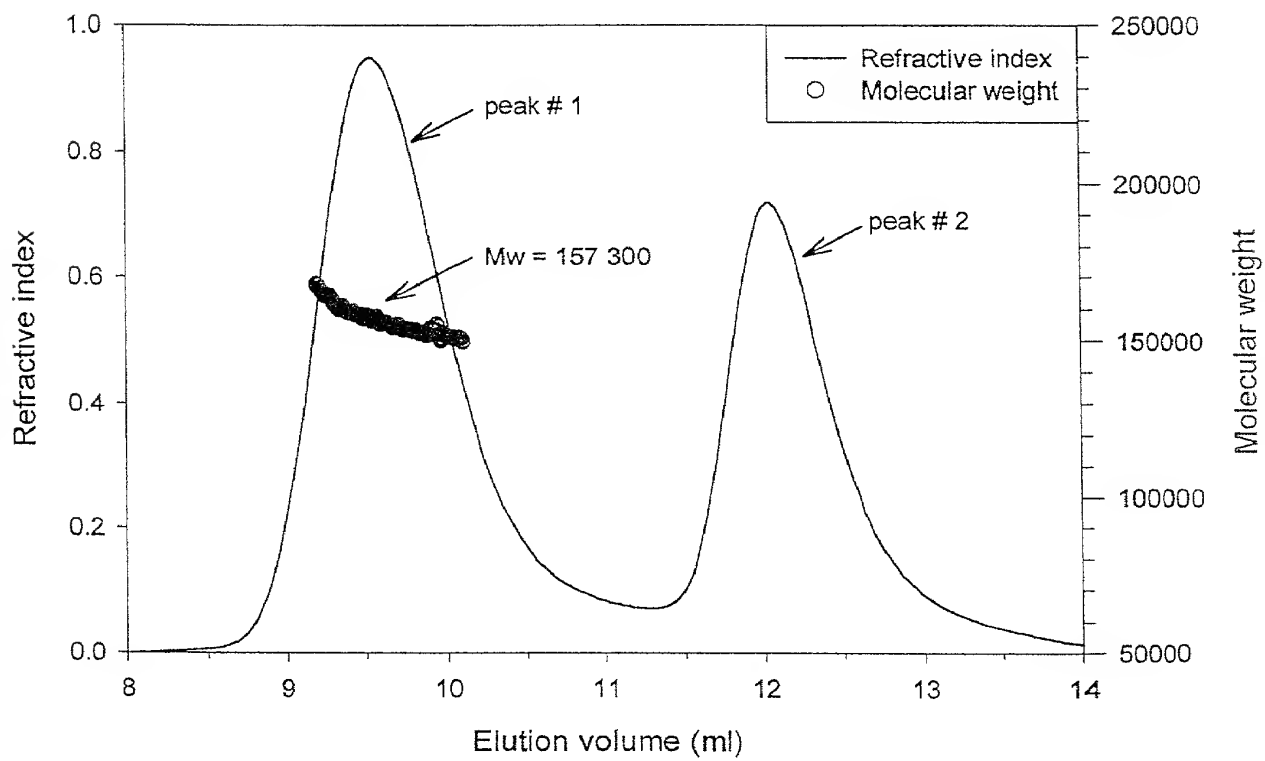


Figure 34

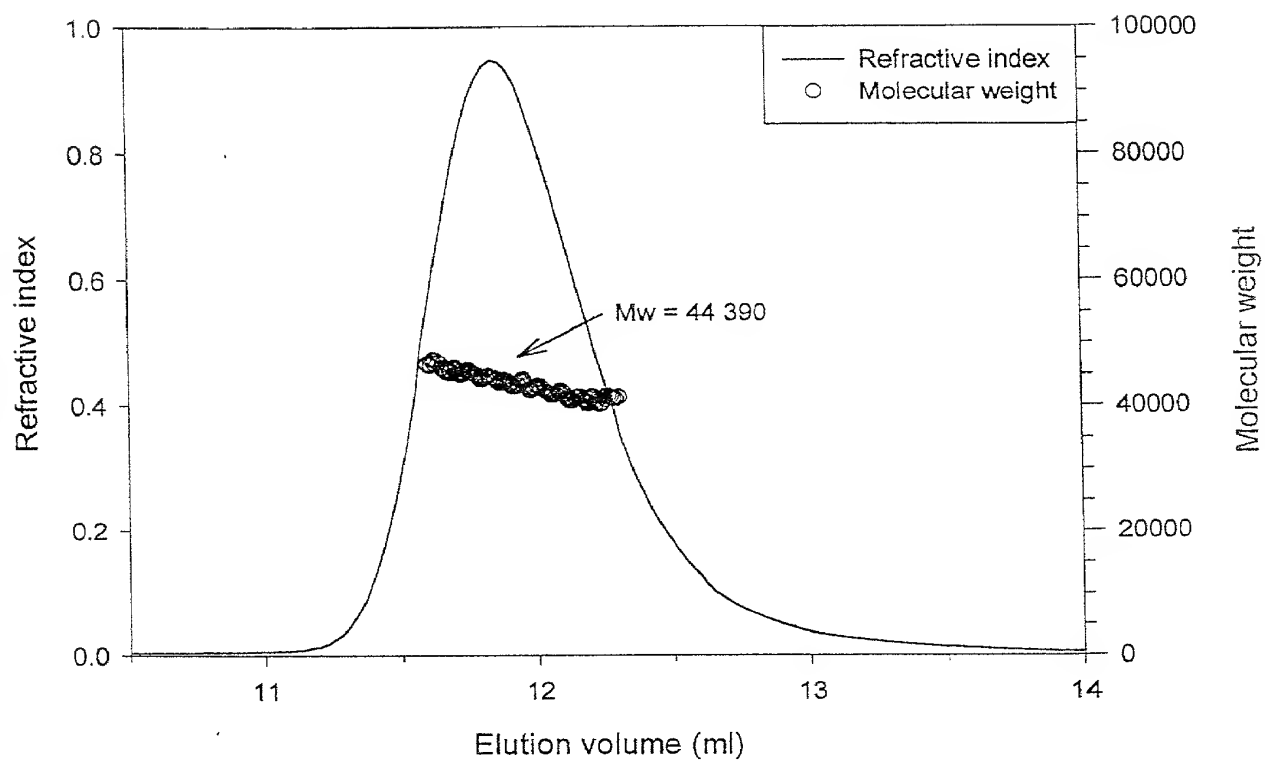


Figure 35

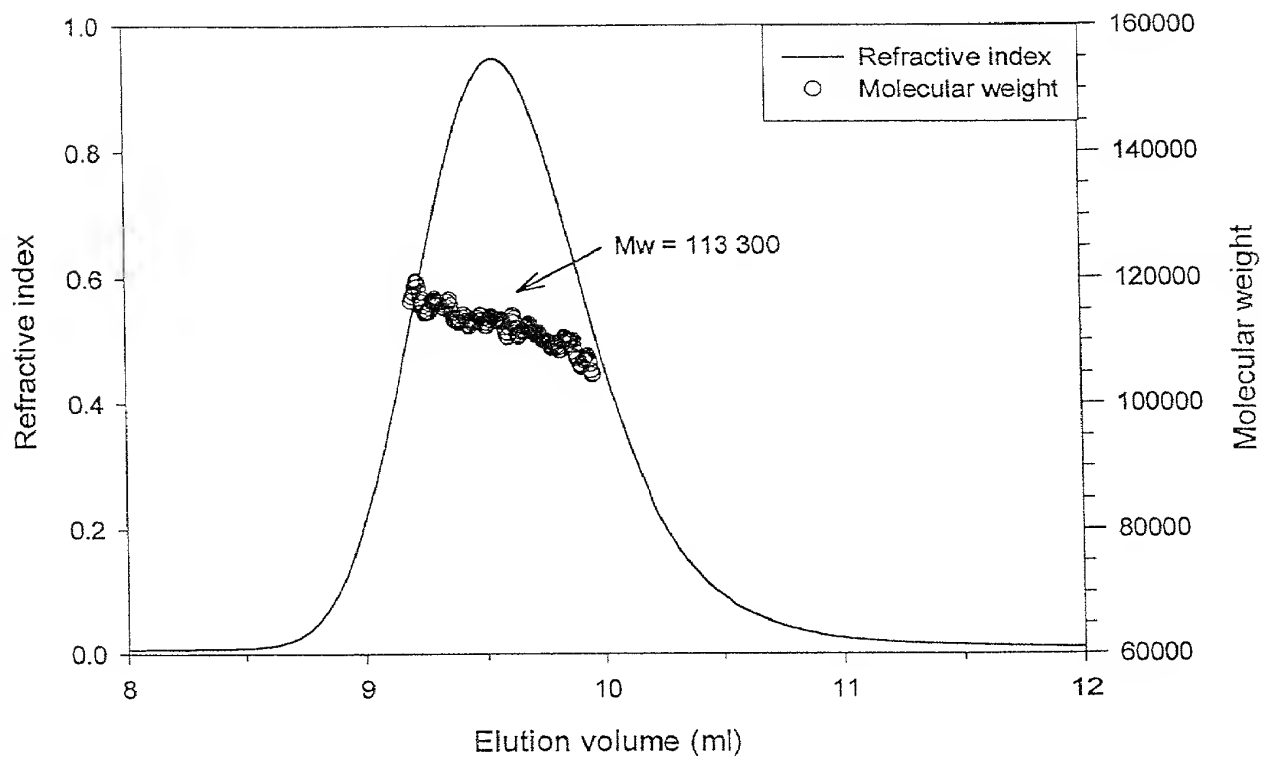


Figure 36

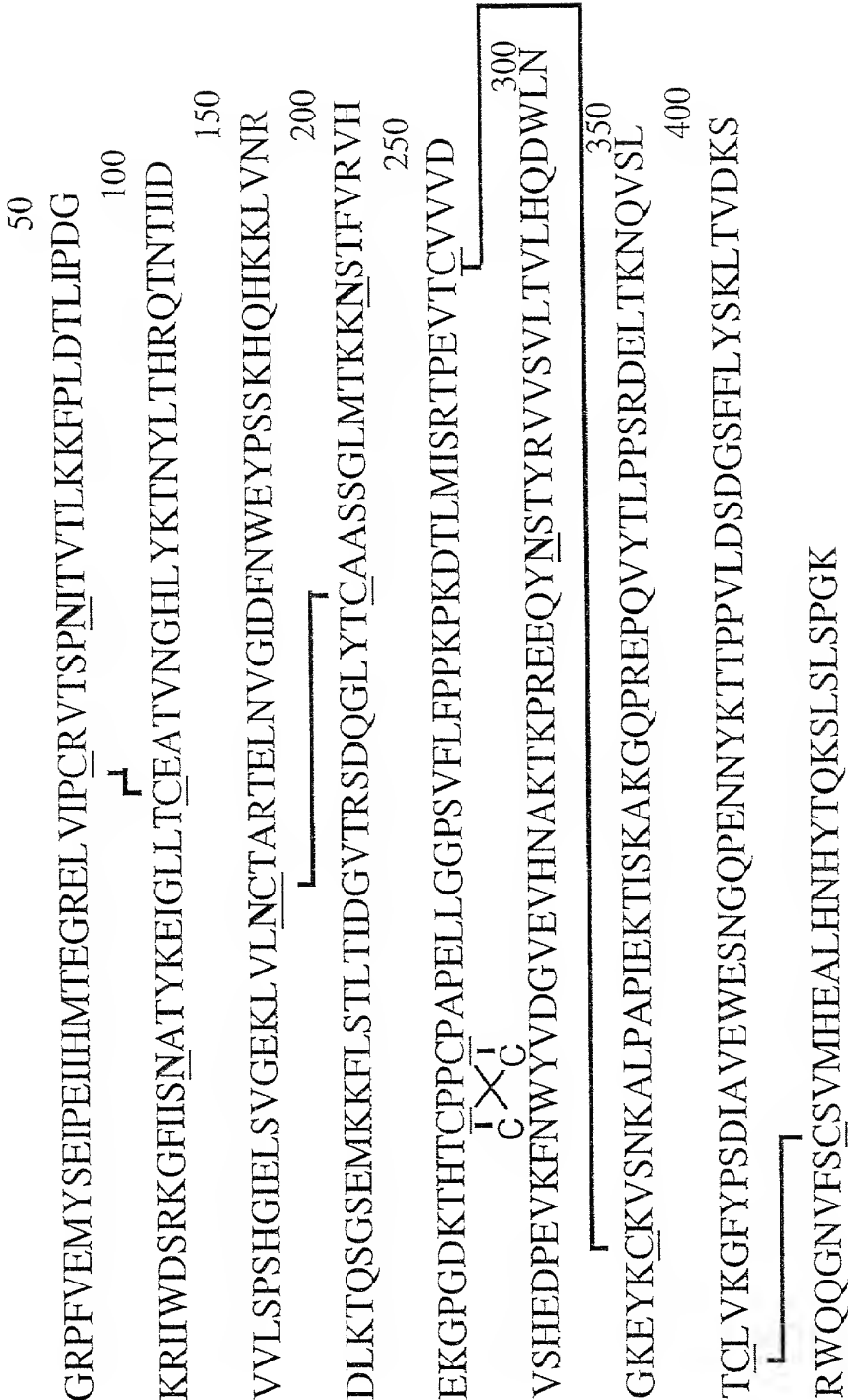


Figure 37

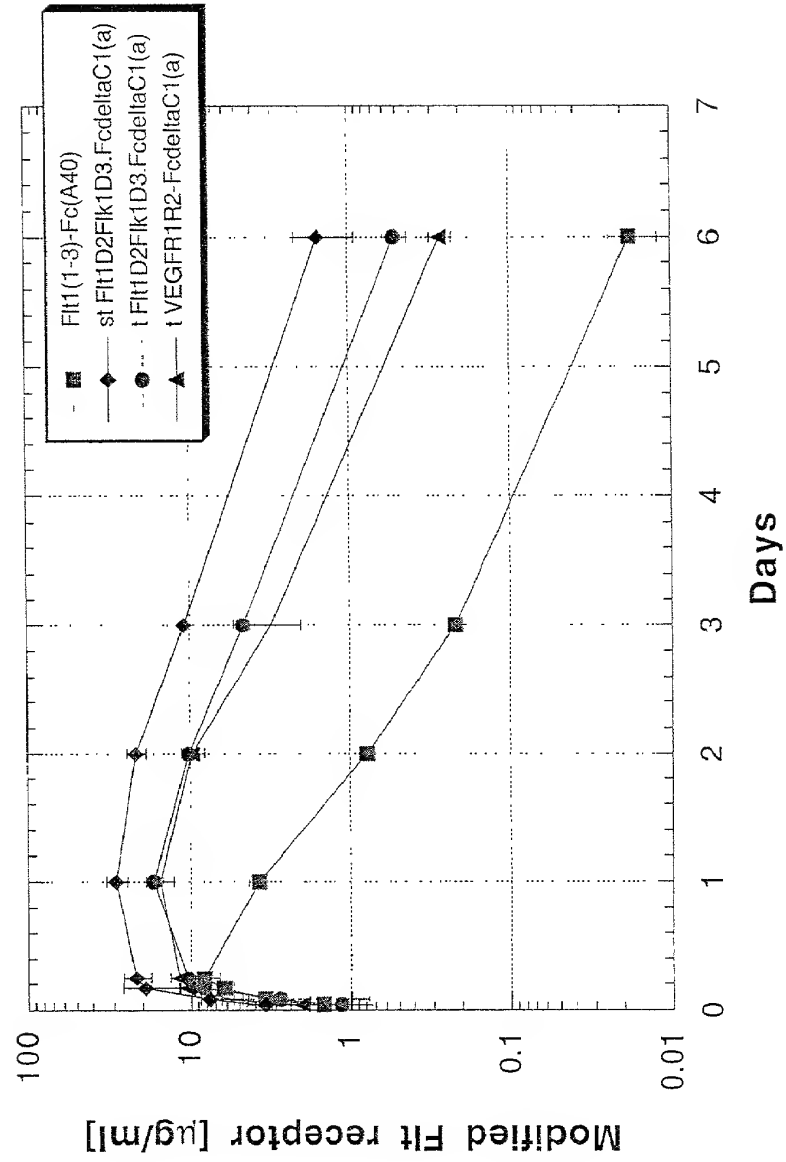


Figure 38

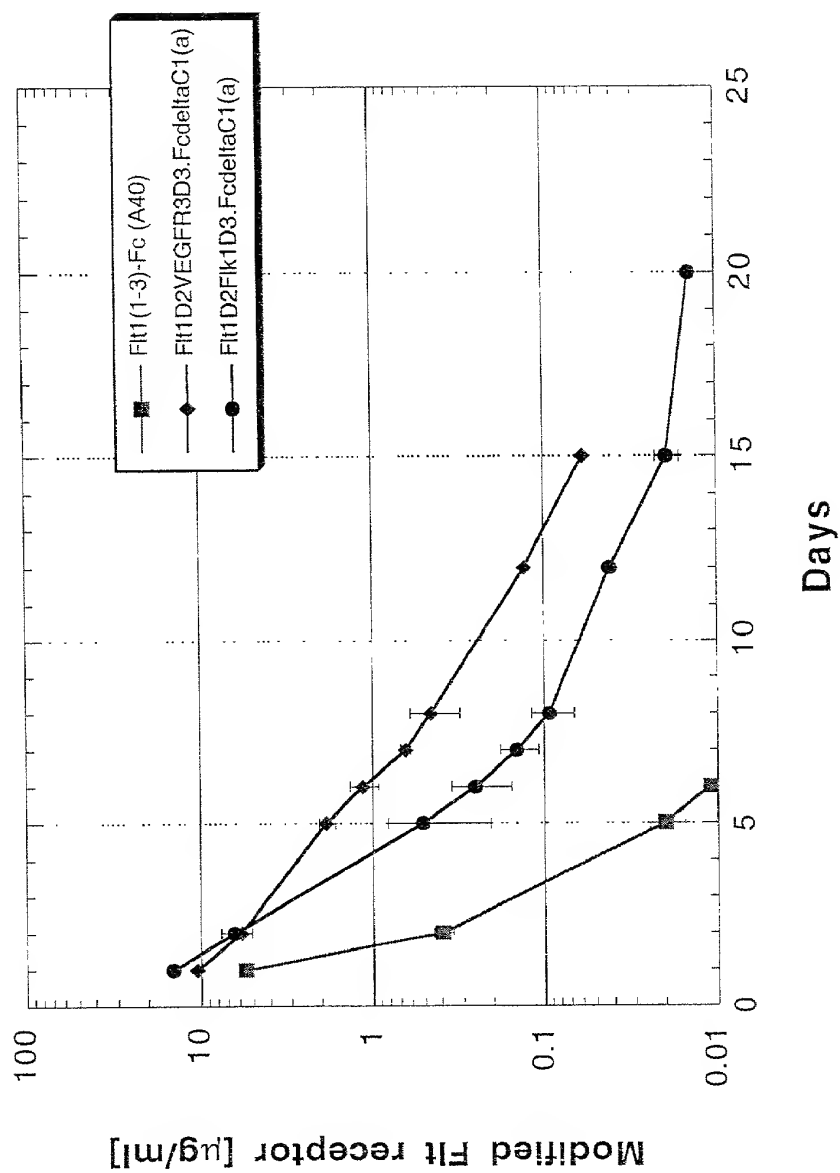


Figure 39

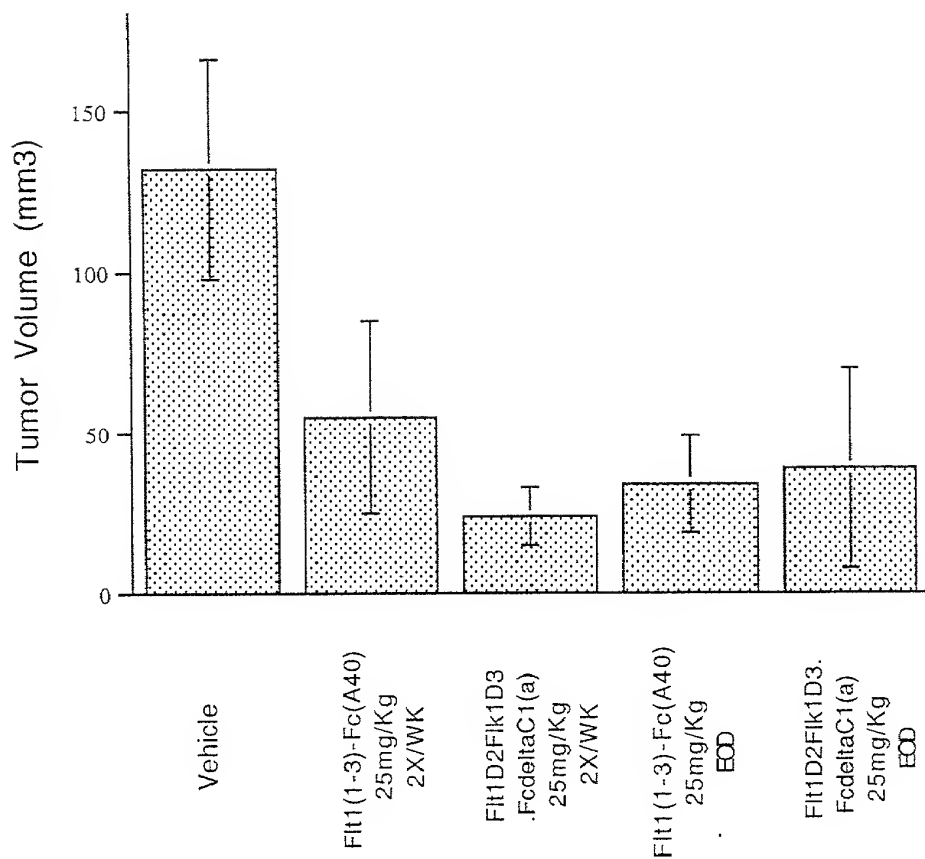


Figure 40

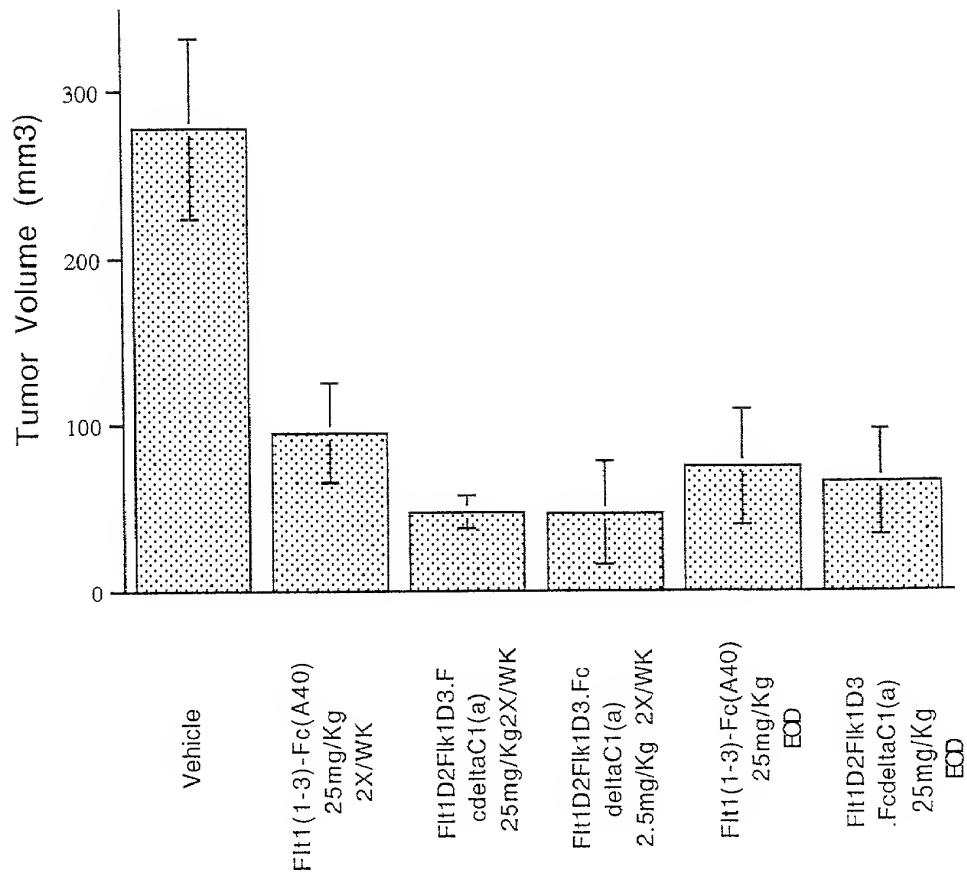


Figure 41

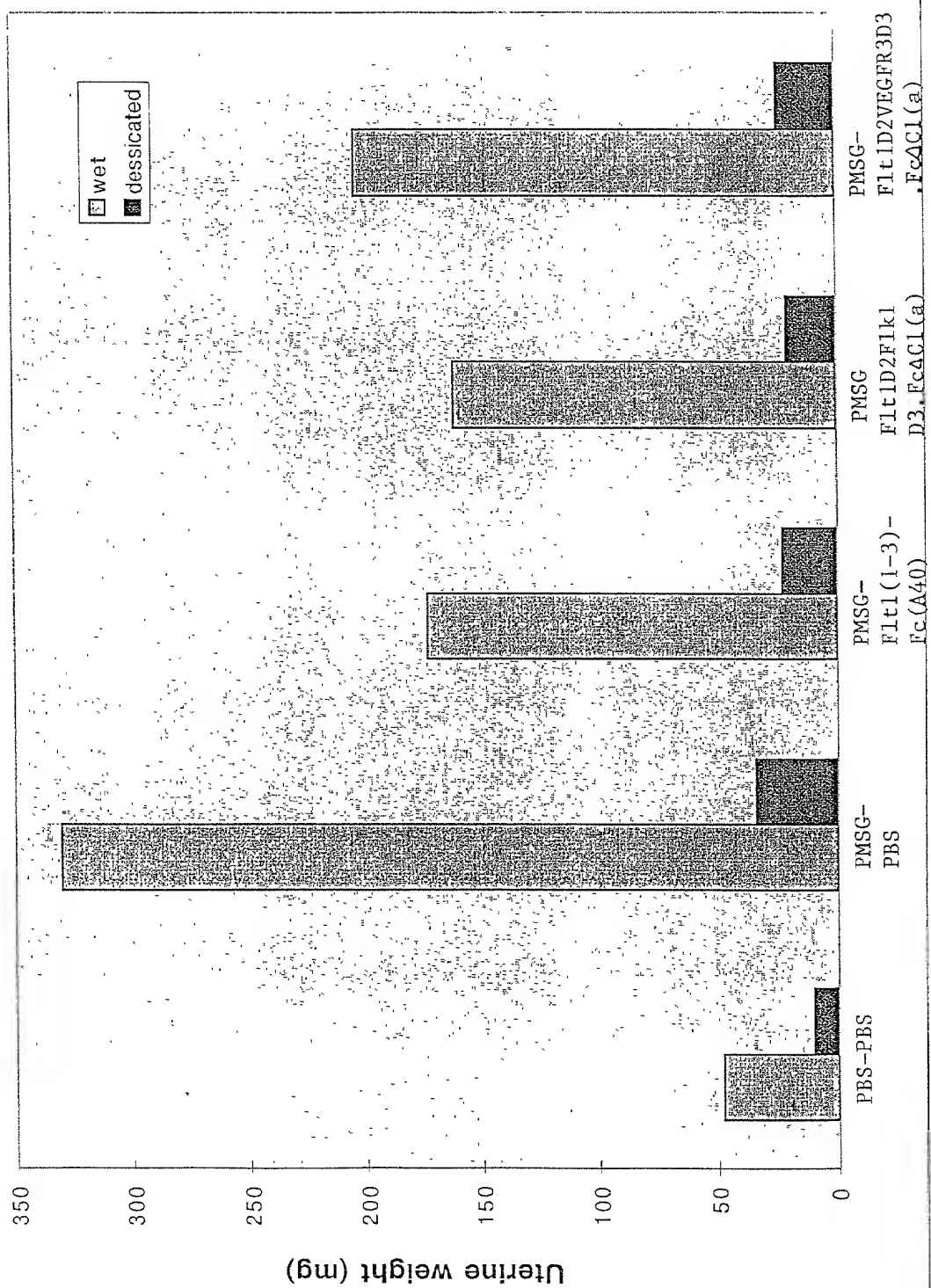


Figure 42A

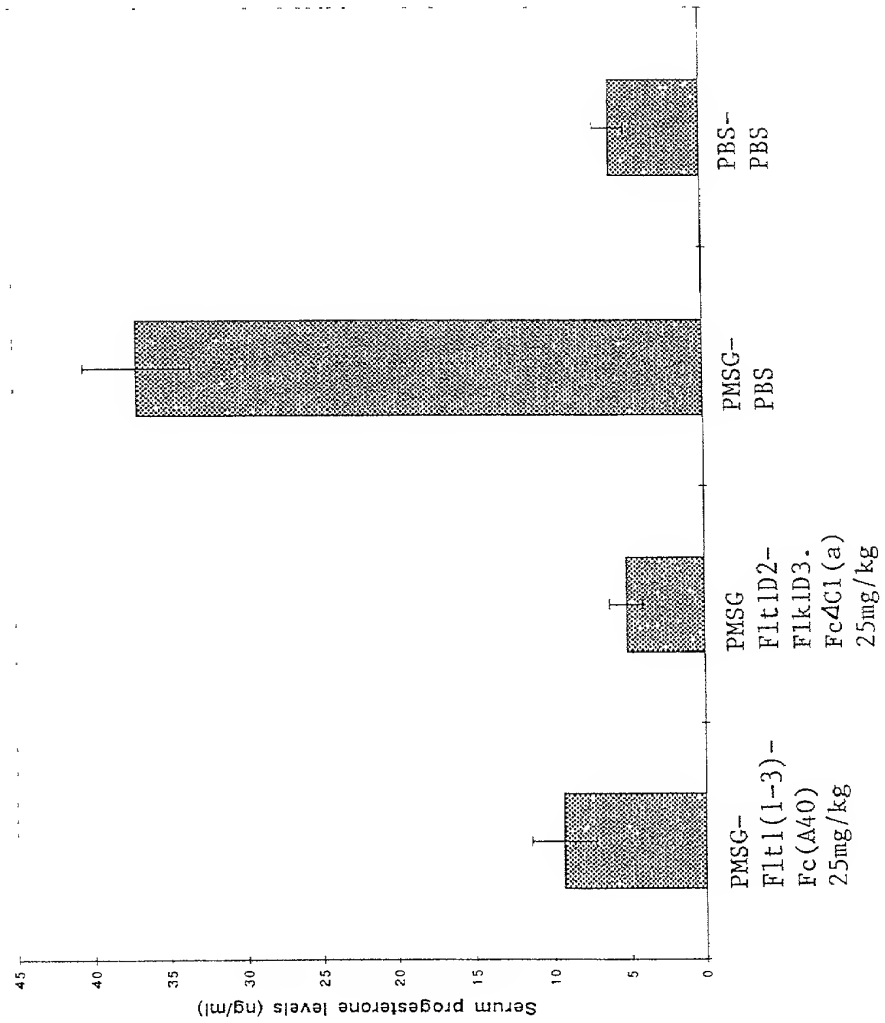


Figure 42B

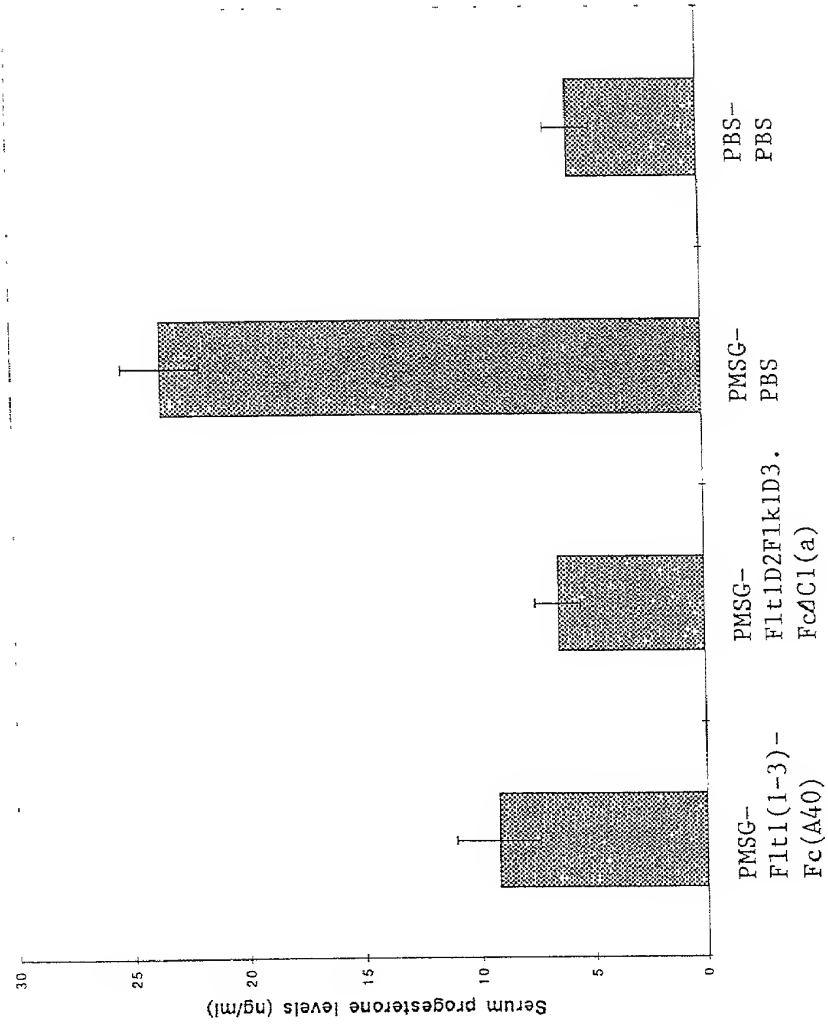


Fig.43



Fig.44 A-C

Fig.44A

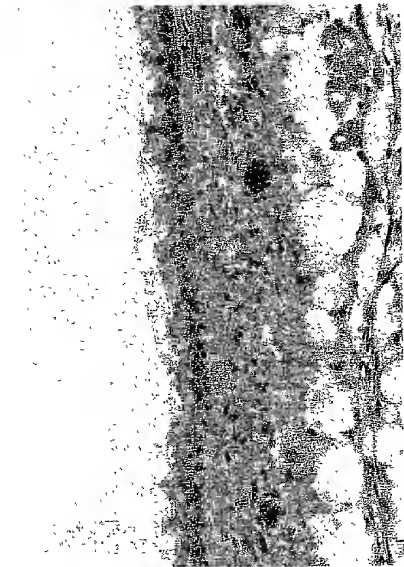


Fig.44B



Fig.44C

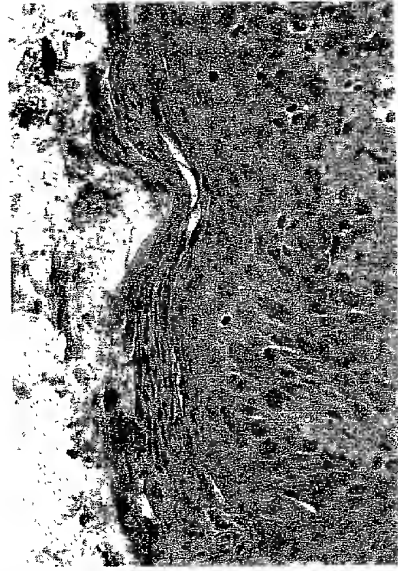


Fig.45



Fig.46 A-B

Fig.46A

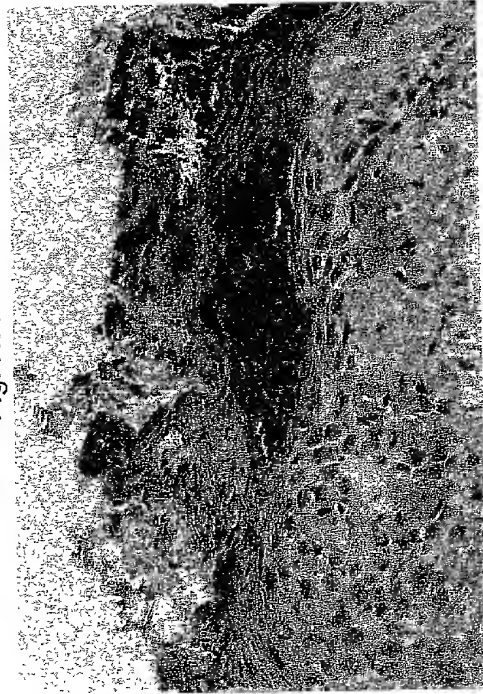


Fig.46B

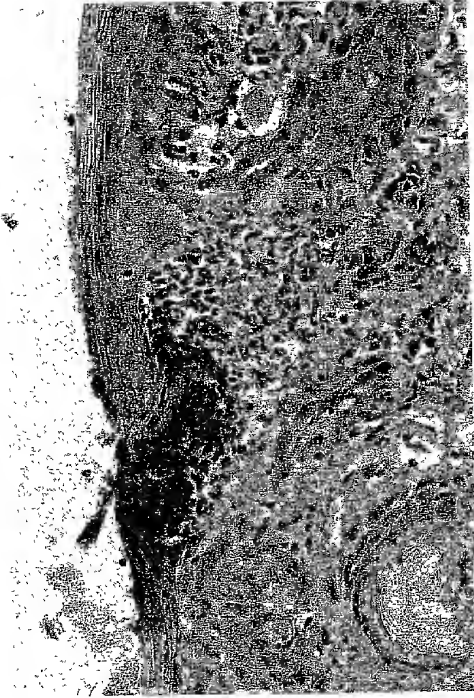


FIGURE 22BEE260

